



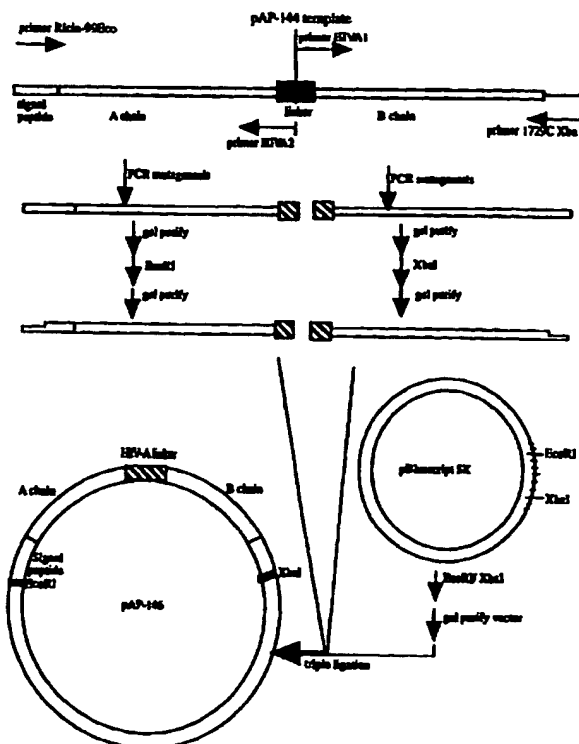
## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>C12N 15/29, 15/62, 15/70, 15/86, A61K 38/16</b>		A1	(11) International Publication Number: <b>WO 97/41233</b>
			(43) International Publication Date: 6 November 1997 (06.11.97)
(21) International Application Number: <b>PCT/CA97/00288</b>		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 29 April 1997 (29.04.97)			
(30) Priority Data: 60/016,509 30 April 1996 (30.04.96) US			
(71) Applicant (for all designated States except US): CANGENE CORPORATION [CA/CA]; 104 Chancellor Matheson Road, Winnipeg, Manitoba R3T 2N2 (CA).			
(72) Inventor; and			
(75) Inventor/Applicant (for US only): BORGFORD, Thor [CA/CA]; 443 Fader Street, New Westminster, British Columbia V3L 3T2 (CA).			
(74) Agent: BERESKIN & PARR; 40th floor, 40 King Street West, Toronto, Ontario M5H 3Y2 (CA).		Published With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.	

## (54) Title: ANTIVIRAL RICIN-LIKE PROTEINS

## (57) Abstract

The present invention provides a protein having an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains. The linker sequence contains a cleavage recognition site for a retroviral protease such as HIV or an HTLV protease. The invention also relates to a nucleic acid molecule encoding the protein and to expression vectors incorporating the nucleic acid molecule. Also provided is a method of inhibiting or destroying mammalian cells infected with a retrovirus utilizing the proteins of the invention; and pharmaceutical compositions for treating HIV infections and human T-cell leukemias involving HTLV.



**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TC	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LJ	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

- 1 -

## Title: Antiviral Ricin-Like Proteins

**FIELD OF THE INVENTION**

5 The invention relates to proteins having A and B chains of a ricin-like toxin, linked by a linker sequence which is specifically cleavable by a retroviral protease to release the active A chain. The invention also relates to a nucleic acid molecule encoding the protein and to expression vectors incorporating the nucleic acid molecule. Also provided is a method of inhibiting or destroying mammalian cells infected with a retrovirus utilizing the proteins of the invention and pharmaceutical compositions for treating HIV infection.

**10 BACKGROUND OF THE INVENTION**

Bacteria and plants are known to produce cytotoxic proteins which may consist of one, two or several polypeptides or subunits. Those proteins having a single subunit may be loosely classified as Type I proteins. Many of the cytotoxins which have evolved two subunit structures are referred to as type II proteins (Saelinger, C.B. in *Trafficking of Bacterial Toxins* (eds. Saelinger, C.B.) 1-13 (CRC Press Inc., Boca Raton, Florida, 1990). One subunit, the A chain, possesses the toxic activity whereas the second subunit, the B chain, binds cell surfaces and mediates entry of the toxin into a target cell. A subset of these toxins kill target cells by inhibiting protein biosynthesis. For example, bacterial toxins such as diphtheria toxin or *Pseudomonas* exotoxin inhibit protein synthesis by inactivating elongation factor 2. Plant toxins such as ricin work by directly inactivating ribosomes [Olsnes, S. & Phil, A. in *Molecular action of toxins and viruses* (eds. Cohen, P. & vanHeyningen, S.); 51-105 (Elsevier Biomedical Press, Amsterdam, 1982).

Ricin, derived from the seeds of *Ricinus communis* (castor oil plant), is the most potent of the plant toxins. It is estimated that a single ricin A chain is able to inactivate ribosomes at a rate of 1500 ribosomes/minute. Consequently, a single molecule of ricin is enough to kill a cell (Olsnes, S. & Phil, A. in *Molecular action of toxins and viruses* (eds. Cohen, P. & vanHeyningen, S.) 51-105 (Elsevier Biomedical Press, Amsterdam, 1982). The ricin toxin is a glycosylated heterodimer with A and B chain molecular masses of 30,625 Da and 31,431 Da respectively. The A chain of ricin has an N-glycosidase activity and catalyzes the excision of a specific adenine residue from the 28S rRNA of eukaryotic ribosomes (Endo, Y; & Tsurugi, K. J. *Biol. Chem.* 262:8128 (1987)). The B chain of ricin, although not toxic in itself, promotes the toxicity of the A chain by binding to galactose residues on the surface of eukaryotic cells and stimulating receptor-mediated endocytosis of the toxin molecule (Simmons et al. *Biol. Chem.* 261:7912 (1986)).

35 Protein toxins are initially produced in an inactive, precursor form. Ricin is initially produced as a single polypeptide (preproricin) with a 35 amino acid N-terminal

- 2 -

presequence and 12 amino acid linker between the A and B chains. The pre-sequence is removed during translocation of the ricin precursor into the endoplasmic reticulum (Lord, J.M. *Eur. J. Biochem.* 146:403-409 (1985) and Lord, J.M. *Eur. J. Biochem.* 146:411-416 (1985)). The proricin is then translocated into specialized organelles called protein bodies  
5 where a plant protease cleaves the protein at a linker region between the A and B chains (Lord, J.M. et al., *FASAB Journal* 8:201-208 (1994)). The two chains, however, remain covalently attached by an interchain disulfide bond (cysteine 259 in the A chain to cysteine 4 in the B chain) and mature disulfide linked ricin is secreted from the plant cells. The A chain is inactive in the proricin (O'Hare, M., et al. *FEBS Lett.* 273:200-204  
10 (1990)) and it is inactive in the disulfide-linked mature ricin (Richardson, P.T., et al. *FEBS Lett.* 255:15-20 (1989)). The ribosomes of the castor bean plant are themselves susceptible to inactivation by ricin A chain; however, as there is no cell surface galactose to permit B chain recognition the A chain cannot re-enter the cell. The exact mechanism of A chain release and activation in target cell cytoplasm is not known (Lord, J.M. et al.,  
15 *FASAB Journal* 8:201-208 (1994)). However, it is known that for activation to take place the disulfide bond between the A and B chains must be reduced and, hence, the linkage between subunits broken.

The ricin gene has been cloned and sequenced, and the X-ray crystal structures of the A and B chains have been described (Rutenber, E., et al. *Proteins* 10:240-250 (1991);  
20 Weston et al., *Mol. Bio.* 244:410-422, 1994; Lamb and Lord *Eur. J. Biochem.* 14:265 (1985); Halling, K., et al. *Nucleic Acids Res.* 13:8019 (1985)). Due to its extreme toxicity there has been much interest in making ricin-based immunotoxins as therapeutic agents for destroying or inhibiting target cells or organisms (Vitetta et al., *Science* 238:1098-1104(1987)). An immunotoxin is a conjugate of a specific cell-binding component, such as a  
25 monoclonal antibody or growth factor and the toxin in which the two protein components are covalently linked. Generally, the components are chemically coupled. However, the linkage may also be a peptide or disulfide bond. The antibody directs the toxin to cell types presenting a specific antigen thereby providing a specificity of action not possible with the natural toxin. Immunotoxins have been made both with the entire ricin molecule  
30 (i.e. both chains) and with the ricin A chain alone ( Spooner et al. *Mol. Immunol.* 31:117-125, (1994)).

Immunotoxins made with the ricin dimer (IT-Rs) are more potent toxins than those made with only the A chain (IT-As). The increased toxicity of IT-Rs is thought to be attributed to the dual role of the B chains in binding to the cell surface and in  
35 translocating the A chain to the cytosolic compartment of the target cell (Vitetta et al., *Science* 238:1098-1104(1987); Vitetta & Thorpe *Seminars in Cell Biology* 2:47-58 (1991)). However, the presence of the B chain in these conjugates also promotes the entry of the

- 3 -

immunotoxin into nontarget cells. Even small amounts of B chain may override the specificity of the cell-binding component as the B chain binds nonspecifically to N-glycosylated galactose, present on most cells. IT-As are more specific and safer to use than IT-Rs. However, in the absence of the B chain the A chain has greatly reduced toxicity.

5 A number of immunotoxins have been designed to recognize antigens on the surfaces of tumour cells. A major problem with the use of ITs is that often the target antigen is also found on non-tumour cells (Vitetta et al., *Immunology Today* 14:252-259 (1993)). Also, due to the reduced potency of IT-As as compared to ITRs, large doses of IT-As must be administered to patients. The large doses frequently cause immune responses and  
10 production of neutralizing antibodies in patients (Vitetta et al., *Science* 238:1098-1104(1987)). IT-As and IT-Rs both suffer from reduced toxicity as the A chain is not released from the conjugate into the target cell cytoplasm.

The insertion of intramolecular cleavage sites between the cytotoxic and cell-binding components of a toxin can mimic the way that the natural toxin is activated.  
15 European patent application no. 466,222 describes the use of maize-derived pro-proteins which can be converted into active form by cleavage with extracellular blood enzymes such as factor Xa, thrombin or collagenase. Westby et al. (*Bioconjugate Chem.*, 3:375-381, 1992) documented fusion proteins which have a specific cell binding component and proricin with a protease sensitive cleavage site specific for factor Xa within the linker  
20 sequence. O'Hare et al. (*FEBS Lett.* 273:200-204, 1990) also describe a recombinant fusion protein of RTA and staphylococcal protein A joined by a trypsin-sensitive cleavage site. In view of the prevalence of the extracellular proteases utilized in these approaches, such artificial activation of the toxin precursor or immunotoxin do not confer a mechanism for intracellular toxin activation, and the problems of target specificity and adverse  
25 immunological reactions to the cell-binding component of the immunotoxin remain.

In view of the extreme toxicity of proteins such as ricin, the lack of specificity of the immunotoxins may severely limit their usefulness as therapeutics for the treatment of cancer and infectious diseases. The preparation of a suitable specific cell binding component may be problematic. For example, antigens specific for the target cell may not  
30 be available and many potential target cells and infective organisms can alter their antigenic make up rapidly to avoid immune recognition.

The potential of bacterial and plant toxins for inhibiting mammalian retroviruses, particularly AIDS, has been investigated. Bacterial toxins such as *Pseudomonas* exotoxin-A and subunit A of diphtheria toxin; dual chain ribosomal inhibitory plant  
35 toxins, such as ricin and single chain ribosomal inhibitory proteins such as trichosanthin and poke weed antiviral protein have been used for the elimination of HIV infected cells (Olson et al. 1991, *AIDS Res. and Human Retroviruses* 7:1025-1030). The high toxicity of

- 4 -

these toxins for mammalian cells, combined with a lack of specificity of action poses a major problem to the development of pharmaceuticals incorporating the toxins, such as immunotoxins.

Immunotoxins are designed such that their specificity of action is determined solely by the antibody component; antigen presenting cells are preferentially destroyed by the drug (Pastan et al., *Annals New York Academy of Sciences* 758:345-353 (1995)). The toxin protein of immunotoxin conjugates does not give the therapeutic any additional specificity of action; it will bring about the destruction of any cell it is delivered to.

#### SUMMARY OF THE INVENTION

The present inventors have prepared novel recombinant toxic proteins which are specifically toxic to cells infected with retroviruses and which do not depend for their specificity of action on a specific cell-binding component. The recombinant proteins of the invention have an A chain of a ricin-like toxin linked to a B chain by a linker sequence, which may be specifically cleaved by a retroviral protease within infected cells to activate the toxic A chain.

In one aspect, the present invention provides a purified and isolated nucleic acid having a nucleotide sequence encoding an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains. The linker sequence is not a linker sequence of a ricin-like toxin, but rather the heterologous linker sequence contains a cleavage recognition site for a retroviral protease. The A and or the B chain may be those of ricin.

In an embodiment, the cleavage recognition site is the cleavage recognition site for an HIV protease. In a particular embodiment, the linker amino acid sequence comprises VSQNYPIVQNFN; SKARVLAEAMSN; or SIRQILFLDGIN. In further particular embodiments, the nucleic acid has the nucleotide sequence shown in Figure 8, Figure 9 or Figure 10.

In another embodiment, the cleavage recognition site is the cleavage recognition site for a human T-cell leukemia virus protease. In a particular embodiment, the linker amino acid sequence comprises SAPQVLPVMHPN or SKTKVLVVQPKN cleaved by a human T-cell leukemia virus-I (HTLV-I) protease; or, SKTKVLVVQPRN or STTQCFPIHPN cleaved by a human T-cell leukemia virus-II (HTLV-II) protease.

The present invention further provides a plasmid incorporating the nucleic acid of the invention. In an embodiment, the plasmid has the restriction map as shown in Figure 1A, 2A, 3A, 16A, 17A, 18A, or 19A.

In another embodiment, the present invention provides a baculovirus transfer vector incorporating the nucleic acid of the invention. In particular embodiments, the invention provides a baculovirus transfer vector having the restriction map as shown in

Figures 5, 6, 7, 16C, 17C, 18C, or 19C or having the DNA sequence as shown in Figure 11.

In a further aspect, the present invention provides a recombinant protein comprising an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains, wherein the linker  
5 sequence contains a cleavage recognition site for a retroviral protease. The A and or the B chain may be those of ricin.

In another aspect, the invention provides a method of inhibiting or destroying mammalian cells infected with a retrovirus having a protease, comprising the steps of preparing a recombinant protein of the invention having a heterologous linker sequence  
10 which contains a cleavage recognition site for the retrovirus protease and introducing the recombinant protein into the cells. In an embodiment, the retrovirus is HIV.

The present invention also relates to a method of treating a mammal infected with HIV by administering the recombinant proteins of the invention to the mammal.

Also provided is a process for preparing a pharmaceutical for treating a mammal  
15 infected with a retrovirus having a protease comprising the steps of preparing a purified and isolated nucleic acid having a nucleotide sequence encoding an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains, wherein the linker sequence contains a cleavage recognition  
20 site for the protease; introducing the nucleic acid into a host cell; expressing the nucleic acid in the host cell to obtain a recombinant protein comprising an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains wherein the linker sequence contains the cleavage recognition site for the protease; and suspending the protein in a pharmaceutically acceptable carrier, diluent or excipient.

In an embodiment, a process is provided for preparing a pharmaceutical for  
25 treating a mammal infected with a retrovirus having a protease comprising the steps of identifying a cleavage recognition site for the protease; preparing a recombinant protein comprising an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains wherein the linker  
30 sequence contains the cleavage recognition site for the protease and suspending the protein in a pharmaceutically acceptable carrier, diluent or excipient.

In a further aspect, the invention provides a pharmaceutical composition for treating a retroviral infection, such as HIV, in a mammal comprising the recombinant  
35 protein of the invention and a pharmaceutically acceptable carrier, diluent or excipient.

The invention also contemplates a method for treating cancer cells containing an HTLV protease comprising (a) preparing a recombinant protein of the invention having a heterologous linker sequence which contains a cleavage recognition site for an HTLV

- 6 -

protease; an (b) introducing the recombinant protein into the cells. The method can be used to treat a mammal with human T-cell leukemias involving HTLV. Compositions for treating human T-cell leukemias involving HTLV comprising the recombinant protein of the invention having a heterologous linker sequence which contains a cleavage recognition site for an HTLV protease, and a pharmaceutically acceptable carrier, diluent, or excipient are also provided.

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples while indicating preferred embodiments of the invention are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

#### **DESCRIPTION OF THE DRAWINGS**

The invention will be better understood with reference to the drawings in which:

Figure 1A summarizes the cloning strategy used to generate the pAP-146 construct;

Figure 1B shows the nucleotide sequence of the HIV-A linker region of pAP-146;

Figure 2A summarizes the cloning strategy used to generate the pAP-147 construct;

Figure 2B shows the nucleotide sequence of the HIV-B linker region of pAP-147;

Figure 3A summarizes the cloning strategy used to generate the pAP-148 construct;

Figure 3B shows the nucleotide sequence of the HIV-H linker region of pAP-148;

Figure 4 shows the amino acid sequences of the wild type ricin linker, the pAP-146 linker, the pAP-147 linker and the pAP-148 linker;

Figure 5 shows the subcloning of the HIV-A linker variant into a baculovirus transfer vector;

Figure 6 shows the subcloning of the HIV-B linker variant into a baculovirus transfer vector;

Figure 7 shows the subcloning of the HIV-H linker variant into a baculovirus transfer vector;

Figure 8 shows the DNA sequence of the pAP-190 insert;

Figure 9 shows the DNA sequence of the pAP-196 insert;

Figure 10 shows the DNA sequence of the pAP-197 insert;

Figure 11 shows the DNA sequence of the baculovirus transfer vector pVL1393;

Figure 12 is a diagram of the vector pSB2;

Figure 13 shows a Western Blot of a pAP-190 proricin variant;

Figure 14 is a blot showing cleavage of a pAP 190 proricin variant by HIV protease;

Figure 15 is a blot showing activation of pAP-190 proricin variant by HIV



- 7 -

protease;

Figure 16A is a diagram summarizing the cloning strategy used to generate the pAP-205 construct;

5 Figure 16B shows the nucleotide sequence of the HTLV-I-A linker regions of pAP-205;

Figure 16C is a diagram showing the subcloning of the HTLV-I-A linker variant into a baculovirus transfer vector;

Figure 16D shows the DNA sequence of the pAP-206 insert containing ricin and the HTLV-I-A linker;

10 Figure 17A is a diagram summarizing the cloning strategy used to generate the pAP-207 construct;

Figure 17B shows the nucleotide sequence of the HTLV-I-B linker regions of pAP-207;

15 Figure 17C is a diagram summarizing the subcloning of the HTLV-I-B linker variant into a baculovirus transfer vector;

Figure 17D shows the DNA sequence of the pAP-208 insert containing ricin and the HTLV-I-B linker;

Figure 18A is a diagram summarizing the cloning strategy used to generate the pAP-209 construct;

20 Figure 18B shows the nucleotide sequence of the HTLV-II-A linker regions of pAP-209;

Figure 18C is a diagram summarizing the subcloning of the HTLV-II-A linker variant into a baculovirus transfer vector;

25 Figure 18D shows the DNA sequence of the pAP-210 insert containing ricin and the HTLV-II-A linker;

Figure 19A is a diagram summarizing the cloning strategy used to generate the pAP-211 construct;

Figure 19B shows the nucleotide sequence of the HTLV-II-B linker regions of pAP-211;

30 Figure 19C is a diagram summarizing the subcloning of the HTLV-II-B linker variant into a baculovirus transfer vector;

Figure 19D shows the DNA sequence of the pAP-212 insert containing ricin and the HTLV-II-B linker; and

35 Figure 20 shows the amino acid sequences of the wild type ricin linker and HTLV protease-sensitive amino acid linkers contained in linkers pAP-205 to pAP-212.

#### **DETAILED DESCRIPTION OF THE INVENTION**

##### **Nucleic Acid Molecules of the Invention**

- 8 -

The present inventors have cloned and expressed novel nucleic acid molecules having a nucleotide sequence encoding an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains. The heterologous linker sequence contains a cleavage recognition site for a retroviral protease  
5 such as a cleavage recognition site for HIV or a human T-cell leukemia virus protease.

The term "isolated and purified" as used herein refers to a nucleic acid substantially free of cellular material or culture medium when produced by recombinant DNA techniques, or chemical precursors, or other chemicals when chemically synthesized. An "isolated and purified" nucleic acid is also substantially free of  
10 sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) from which the nucleic acid is derived. The term "nucleic acid" is intended to include DNA and RNA and can be either double stranded or single stranded.

The term "linker sequence" as used herein refers to an internal amino acid sequence within the protein encoded by the nucleic acid molecule of the invention which contains  
15 residues linking the A and B chain so as to render the A chain incapable of exerting its toxic effect, for example catalytically inhibiting translation of a eukaryotic ribosome. By heterologous is meant that the linker sequence is not a sequence native to the A or B chain of a ricin-like toxin or precursor thereof. However, preferably, the linker sequence may be of a similar length to the linker sequence of a ricin-like toxin and should not  
20 interfere with the role of the B chain in cell binding and transport into the cytoplasm. When the linker sequence is cleaved the A chain becomes active or toxic.

The nucleic acid molecule of the invention was cloned by subjecting a preproricin cDNA clone (pAP-144) to site-directed mutagenesis in order to generate a series of variants differing only in the sequence between the A and B chains (linker region).  
25 Oligonucleotides, corresponding to the extreme 5' and 3' ends of the preproricin gene were synthesized and used to PCR amplify the gene. Using the cDNA sequence for preproricin (Lamb et al., Eur. J. Biochem., 145:266-270, 1985), several oligonucleotide primers were designed to flank the start and stop codons of the preproricin open reading frame.

The preproricin cDNA was amplified using the upstream primer Ricin-99 (or  
30 Ricin-109 may be used) and the downstream primer Ricin1729C with Vent DNA polymerase (New England Biolabs) using standard procedures (Sambrook et al., Molecular Cloning: A Laboratory Manual, Second Edition, (Cold Spring Harbor Laboratory Press, 1989)). The use of the upstream primer Ricin-109 circumvents the subcloning step into vector pSB2. The purified PCR fragment encoding the preproricin  
35 cDNA was then ligated into an Eco RV-digested pBluescript II SK plasmid (Stratagene), and used to transform competent XL1-Blue cells (Stratagene).

The cloned PCR product containing the putative preproricin gene was confirmed by

DNA sequencing of the entire cDNA clone (pAP-144). The sequences and location of oligonucleotide primers used for sequencing are shown in Table 1.

5 The preproricin cDNA clone (pAP-144) was subjected to site-directed mutagenesis in order to generate a series of variants differing only in the sequence between the A and B chains (linker region). The wild-type preproricin linker region was replaced with the three linker sequences, pAP-146, pAP-147 and pAP-148 shown in Figure 4. The linker regions of the variants encode an HIV protease cleavage recognition sequence (Slalka et al., Cell, 56:911-913, 1989). The mutagenesis and cloning strategy used to generate the linker variants pAP-146, pAP-147 and pAP-148 are summarized in Figures 1A and 1B, 2A and 2B and 3A and 3B respectively. The first step involved a DNA amplification using a set of mutagenic primers (HIVA 1, 2; HIVB 1, 2; HIVH 1, 2) in combination with the two flanking primers Ricin-99Eco and Ricin1729Xba. Restriction digested PCR fragments were gel purified and then ligated with PBluescript SK which had been digested with Eco RI and Xba I. Ligation reactions were used to transform competent XL1-Blue cells (Stratagene). Recombinant clones were identified by restriction digests of plasmid miniprep DNA and the mutant linker sequences were confirmed by DNA sequencing.

10 Recombinant clones were subcloned into vector pSB2. The three constructs obtained were pAP-151, pAP-159, and pAP-163, with each having the mutant linker found in pAP-146, pAP-147, and pAP-148 respectively.

20 The cloning strategy described above may also be applied to the preparation of recombinant clones containing a cleavage recognition site for a human T-cell leukemia virus protease. For example, recombinant clones pAP-205, pAP-207, pAP-209, and pAP-211 were prepared using a method similar to the one described above.

25 The nucleic acid molecule of the invention has sequences encoding an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker sequence containing a cleavage recognition site for a retroviral protease, such as an HIV protease or an HTLV protease. The nucleic acid may be expressed to provide a recombinant protein having an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker sequence containing a cleavage recognition site for a retroviral protease, such as an HIV protease or an HTLV protease.

30 The nucleic acid molecule may comprise the A and/or B chain of ricin. The ricin gene has been cloned and sequenced, and the X-ray crystal structures of the A and B chains are published (Rutenber, E., et al. Proteins 10:240-250 (1991); Weston et al., Mol. Bio. 244:410-422, 1994; Lamb and Lord Eur. J. Biochem. 14:265 (1985); Halling, K., et al. Nucleic Acids Res. 13:8019 (1985)). It will be appreciated that the invention includes nucleic acid molecules encoding truncations of A and B chains of ricin-like proteins and analogs and homologs of A and B chains of ricin-like proteins and truncations thereof (i.e., ricin-like

- 10 -

proteins), as described herein. It will further be appreciated that variant forms of the nucleic acid molecules of the invention which arise by alternative splicing of an mRNA corresponding to a cDNA of the invention are encompassed by the invention.

Another aspect of the invention provides a nucleotide sequence which hybridizes  
5 under high stringency conditions to a nucleotide sequence encoding the A and/or B chains of a ricin-like protein. Appropriate stringency conditions which promote DNA hybridization are known to those skilled in the art, or can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C may  
10 be employed. The stringency may be selected based on the conditions used in the wash step. By way of example, the salt concentration in the wash step can be selected from a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be at high stringency conditions, at about 65°C.

The nucleic acid molecule may comprise the A and/or B chain of a ricin-like toxin.  
15 Methods for cloning ricin-like toxins are known in the art and are described, for example, in E.P. 466,222. Sequences encoding ricin or ricin-like A and B chains may be obtained by selective amplification of a coding region, using sets of degenerative primers or probes for selectively amplifying the coding region in a genomic or cDNA library. Appropriate primers may be selected from the nucleic acid sequence of A and B chains of ricin or ricin-  
20 like toxins. It is also possible to design synthetic oligonucleotide primers from the nucleotide sequences for use in PCR. Suitable primers may be selected from the sequences encoding regions of ricin-like proteins which are highly conserved, as described for example in U.S. Patent No 5,101,025 and E.P. 466,222.

A nucleic acid can be amplified from cDNA or genomic DNA using these  
25 oligonucleotide primers and standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. It will be appreciated that cDNA may be prepared from mRNA, by isolating total cellular mRNA by a variety of techniques, for example, by using the guanidinium-thiocyanate extraction procedure of Chirgwin et al., Biochemistry, 18, 5294-5299 (1979).  
30 cDNA is then synthesized from the mRNA using reverse transcriptase (for example, Moloney MLV reverse transcriptase available from Gibco/BRL, Bethesda, MD, or AMV reverse transcriptase available from Seikagaku America, Inc., St. Petersburg, FL).

It will be appreciated that the methods described above may be used to obtain the coding sequence from plants, bacteria or fungi, preferably plants, which produce known ricin-like  
35 proteins and also to screen for the presence of genes encoding as yet unknown ricin-like proteins.

A sequence containing a cleavage recognition site for a retroviral protease may be

selected based on the retrovirus which is to be targeted by the recombinant protein. The cleavage recognition site may be selected from sequences known to encode a cleavage recognition site for the retrovirus protease. Sequences encoding cleavage recognition sites may be identified by testing the expression product of the sequence for susceptibility to cleavage by a retroviral protease. An assay to identify peptides having cleavage recognition sites for HIV protease is described in PCT/US88/01849. The HIV protease encoded by the p17 gene of HIV and has the highly conserved Asp-Thr-Gly sequence characteristic of the active site of cellular aspartyl proteases. The HIV protease may be prepared by methods known in the art and used to test suspected cleavage recognition sites. For example, a polypeptide containing the suspected cleavage recognition site may be incubated with the protease and the amount of cleavage product determined (DiIanni, 1990, J. Biol. Chem. 285: 17345-17354). Substrates for HIV proteases are described in U.S. Patent No. 5,235,039. The invention is not restricted to proteins including the cleavage recognition site for HIV proteases, but includes recognition sites of other retroviral proteases, including proteases of members of the subfamilies oncovirinae, lentivirinae and spumavirinae for example from HTLV, AMV, RSV, BLV, FeLV and MMTV. Examples of retroviral proteases and conserved sequences thereof are provided, for example, in Katoh et al., (Nature 329:654-656).

A sequence containing a cleavage recognition site for an HTLV protease may be selected using the conventional methods described herein. The preparation of human T-cell leukemia virus proteases, their substrates and enzymatic activity assay methodology have been described by Petit, S.C. et al. (J. Biol. Chem. 266:14539-14547 (1991)) and Blaha, I. et al. (FEBS Lett. 309:389-393 (1992)).

In an embodiment, the cleavage recognition site is the cleavage recognition site for an HIV protease. In a particular embodiment, the linker amino acid sequence comprises VSQNYPIVQNFN; SKARVLAEAMSN; or SIKILFLDGIN. In further particular embodiments, the nucleic acid has the nucleotide sequence shown in Figure 8, Figure 9 or Figure 10.

In another embodiment, the cleavage recognition site is the cleavage recognition site for a human T-cell leukemia virus protease. In a particular embodiment, the linker amino acid sequence comprises SAPQVLPVMHPN or SKTKVLVVQPKN cleaved by a human T-cell leukemia virus-I (HTLV-I) protease; or, SKTKVLVVQPRN or STTQCFPIHPN cleaved by a human T-cell leukemia virus-II (HTLV-II) protease.

The nucleic acid molecule of the invention may be prepared by site directed mutagenesis. For example, the cleavage site of a retroviral protease may be prepared by site directed mutagenesis of the homologous linker sequence of a proricin-like toxin. Procedures for cloning proricin-like genes, encoding a linker sequence are described in EP

- 12 -

466,222. Site directed mutagenesis may be accomplished by DNA amplification of mutagenic primers in combination with flanking primers. Suitable procedures using the mutagenic primers HIVA1, HIVB1 and HIVH1 are shown in Figures 1A to 3B, and Figures 16A, 16B, 17A, 17B, 18A, 19A and 19B.

5       The nucleic acid molecule of the invention may also encode a fusion protein. A sequence encoding a heterologous linker sequence containing a cleavage recognition site for a retroviral protease may be cloned from a cDNA or genomic library or chemically synthesized based on the known sequence of such cleavage sites. The heterologous linker sequence may then be fused in frame with the sequences encoding the A and B chains of the  
10       ricin-like toxin for expression as a fusion protein. It will be appreciated that a nucleic acid molecule encoding a fusion protein may contain a sequence encoding an A chain and a B chain from the same ricin-like toxin or the encoded A and B chains may be from different toxins. For example, the A chain may be derived from ricin and the B chain may be derived from abrin. A protein may also be prepared by chemical conjugation of the A  
15       and B chains and linker sequence using conventional coupling agents for covalent attachment.

      An isolated and purified nucleic acid molecule of the invention which is RNA can be isolated by cloning a cDNA encoding an A and B chain and a linker into an appropriate vector which allows for transcription of the cDNA to produce an RNA molecule which  
20       encodes a protein of the invention. For example, a cDNA can be cloned downstream of a bacteriophage promoter, (e.g. a T7 promoter) in a vector, cDNA can be transcribed in vitro with T7 polymerase, and the resultant RNA can be isolated by standard techniques.

#### Recombinant Protein of the Invention

      As previously mentioned, the invention provides novel recombinant proteins  
25       which incorporate the A and B chains of a ricin-like toxin linked by a heterologous linker sequence containing a cleavage recognition site for a retroviral protease, such as an HIV protease or an HTLV protease. It is an advantage of the recombinant proteins of the invention that they are non-toxic until the A chain is liberated from the B chain by specific cleavage of the linker by the retroviral protease, such as an HIV protease or an  
30       HTLV protease. Thus the protein may be used to specifically target cells infected with the retrovirus in the absence of additional specific cell-binding components to target infected cells. It is a further advantage that the retroviral protease cleaves the heterologous linker intracellularly thereby releasing the toxic A chain directly into the cytoplasm of the infected cell. As a result, infected cells are specifically targeted and  
35       non-infected cells are not directly exposed to the activated free A chain.

      Ricin is a plant derived ribosome inhibiting protein which blocks protein synthesis in eukaryotic cells. Ricin may be derived from the seeds of *Ricinus communis*

- 13 -

(castor oil plant). The ricin toxin is a glycosylated heterodimer with A and B chain molecular masses of 30,625 Da and 31,431 Da respectively. The A chain of ricin has an N-glycosidase activity and catalyzes the excision of a specific adenine residue from the 28S rRNA of eukaryotic ribosomes (Endo, Y; & Tsurugi, K. *J. Biol. Chem.* 262:8128 (1987)). The B chain of ricin, although not toxic in itself, promotes the toxicity of the A chain by binding to galactose residues on the surface of eukaryotic cells and stimulating receptor-mediated endocytosis of the toxin molecule (Simmons et al. *Biol. Chem.* 261:7912 (1986)).

Protein toxins are initially produced in an inactive, precursor form. Ricin is initially produced as a single polypeptide (preproricin) with a 35 amino acid N-terminal presequence and 12 amino acid linker between the A and B chains. The pre-sequence is removed during translocation of the ricin precursor into the endoplasmic reticulum (Lord, J.M. *Eur. J. Biochem.* 146:403-409 (1985) and Lord, J.M. *Eur. J. Biochem.* 146:411-416 (1985)). The proricin is then translocated into specialized organelles called protein bodies where a plant protease cleaves the protein at a linker region between the A and B chains (Lord, J.M. et al., *FASAB Journal* 8:201-208 (1994)). The two chains, however, remain covalently attached by an interchain disulfide bond (cysteine 259 in the A chain to cysteine 4 in the B chain) and mature disulfide linked ricin is secreted from the plant cells. The A chain is inactive in the proricin (O'Hare, M., et al. *FEBS Lett.* 273:200-204 (1990)) and it is inactive in the disulfide-linked mature ricin (Richardson, P.T., et al. *FEBS Lett.* 255:15-20 (1989)). The ribosomes of the castor bean plant are themselves susceptible to inactivation by ricin A chain; however, as there is no cell surface galactose to permit B chain recognition the A chain cannot re-enter the cell.

Ricin-like proteins include bacterial, fungal and plant toxins which have A and B chains and inactivate ribosomes and inhibit protein synthesis. The A chain is an active polypeptide subunit which is responsible for the pharmacologic effect of the toxin. In most cases the active component of the A chain is an enzyme. The B chain is responsible for binding the toxin to the cell surface and is thought to facilitate entry of the A chain into the cell cytoplasm. The A and B chains in the mature toxins are linked by disulfide bonds. The toxins most similar in structure to ricin are plant toxins which have one A chain and one B chain. Examples of such toxins include abrin which may be isolated from the seeds of *Abrus precatorius*, ricin which may be isolated from the seeds of castor beans *Ricinus communis*, and modeccin.

Ricin-like bacterial proteins include diphtheria toxin, which is produced by *Corynebacterium diphtheriae*, *Pseudomonas* enterotoxin A and cholera toxin. It will be appreciated that the term ricin-like toxins is also intended to include the A chain of those toxins which have only an A chain. The recombinant proteins of the invention could include the A chain of these toxins conjugated to, or expressed as, a recombinant protein

- 14 -

with the B chain of another toxin. Examples of plant toxins having only an A chain include trichosanthin, MMC and pokeweed antiviral proteins, dianthin 30, dianthin 32, crotin II, curcin II and wheat germ inhibitor. Examples of fungal toxins having only an A chain include alpha-sarcin, restrictocin, mitogillin, enomycin, phenomycin. Examples of bacterial toxins having only an A chain include cytotoxin from *Shigella dysenteriae* and related Shiga-like toxins. Recombinant trichosanthin and the coding sequence thereof is disclosed in U.S. Patents Nos. 5,101,025 and 5,128,460.

In addition to the entire B or A chains of a ricin-like toxin, it will be appreciated that the recombinant protein of the invention may contain only that portion of the A chain which is necessary for exerting its cytotoxic effect. For example, the first 30 amino acids of the ricin A chain may be removed resulting in a truncated A chain which retains toxic activity. The truncated ricin or ricin-like A chain may be prepared by expression of a truncated gene or by proteolytic degradation, for example with Nagarase (Funmatsu et al., 1970, Jap. J. Med. Sci. Biol. 23:264-267). Similarly, the recombinant protein of the invention may contain only that portion of the B chain necessary for galactose recognition, cell binding and transport into the cell cytoplasm. Truncated B chains are described for example in EP 145,111. The A and B chains may be glycosylated or non-glycosylated. Glycosylated A and B chains may be obtained by expression in the appropriate host cell capable of glycosylation. Non-glycosylated chains may be obtained by expression in nonglycosylating host cells or by treatment to remove or destroy the carbohydrate moieties.

The proteins of the invention may be prepared using recombinant DNA methods. Accordingly, the nucleic acid molecules of the present invention may be incorporated in a known manner into an appropriate expression vector which ensures good expression of the protein. Possible expression vectors include but are not limited to cosmids, plasmids, or modified viruses (e.g. replication defective retroviruses, adenoviruses and adeno-associated viruses), so long as the vector is compatible with the host cell used. The expression vectors are "suitable for transformation of a host cell", means that the expression vectors contain a nucleic acid molecule of the invention and regulatory sequences selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid molecule. Operatively linked is intended to mean that the nucleic acid is linked to regulatory sequences in a manner which allows expression of the nucleic acid.

The invention therefore contemplates a recombinant expression vector of the invention containing a nucleic acid molecule of the invention, or a fragment thereof, and the necessary regulatory sequences for the transcription and translation of the inserted protein-sequence. Suitable regulatory sequences may be derived from a variety of sources,



- 15 -

including bacterial, fungal, viral, mammalian, or insect genes (For example, see the regulatory sequences described in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990). Selection of appropriate regulatory sequences is dependent on the host cell chosen as discussed below, and may be readily accomplished by one of ordinary skill in the art. Examples of such regulatory sequences include: a transcriptional promoter and enhancer or RNA polymerase binding sequence, a ribosomal binding sequence, including a translation initiation signal. Additionally, depending on the host cell chosen and the vector employed, other sequences, such as an origin of replication, additional DNA restriction sites, enhancers, and sequences conferring inducibility of transcription may be incorporated into the expression vector. It will also be appreciated that the necessary regulatory sequences may be supplied by the native A and B chains and/or its flanking regions.

The recombinant expression vectors of the invention may also contain a selectable marker gene which facilitates the selection of host cells transformed or transfected with a recombinant molecule of the invention. Examples of selectable marker genes are genes encoding a protein such as G418 and hygromycin which confer resistance to certain drugs,  $\beta$ -galactosidase, chloramphenicol acetyltransferase, firefly luciferase, or an immunoglobulin or portion thereof such as the Fc portion of an immunoglobulin preferably IgG. Transcription of the selectable marker gene is monitored by changes in the concentration of the selectable marker protein such as  $\beta$ -galactosidase, chloramphenicol acetyltransferase, or firefly luciferase. If the selectable marker gene encodes a protein conferring antibiotic resistance such as neomycin resistance transformant cells can be selected with G418. Cells that have incorporated the selectable marker gene will survive, while the other cells die. This makes it possible to visualize and assay for expression of recombinant expression vectors of the invention and in particular to determine the effect of a mutation on expression and phenotype. It will be appreciated that selectable markers can be introduced on a separate vector from the nucleic acid of interest.

The recombinant expression vectors may also contain genes which encode a fusion moiety which provides increased expression of the recombinant protein; increased solubility of the recombinant protein; and aid in the purification of the target recombinant protein by acting as a ligand in affinity purification. For example, a proteolytic cleavage site may be added to the target recombinant protein to allow separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Typical fusion expression vectors include pGEX (Amrad Corp., Melbourne, Australia), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E

- 16 -

binding protein, or protein A, respectively, to the recombinant protein.

Recombinant expression vectors can be introduced into host cells to produce a transformant host cell. The term "transformant host cell" is intended to include prokaryotic and eukaryotic cells which have been transformed or transfected with a recombinant expression vector of the invention. The terms "transformed with",  
5 "transfected with", "transformation" and "transfection" are intended to encompass introduction of nucleic acid (e.g. a vector) into a cell by one of many possible techniques known in the art. Prokaryotic cells can be transformed with nucleic acid by, for example, electroporation or calcium-chloride mediated transformation. Nucleic acid can be  
10 introduced into mammalian cells via conventional techniques such as calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofectin, electroporation or microinjection. Suitable methods for transforming and transfecting host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory press (1989)), and other laboratory textbooks.

15 Suitable host cells include a wide variety of prokaryotic and eukaryotic host cells. For example, the proteins of the invention may be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus), yeast cells or mammalian cells. Other suitable host cells can be found in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1991).

20 More particularly, bacterial host cells suitable for carrying out the present invention include *E. coli*, *B. subtilis*, *Salmonella typhimurium*, and various species within the genus' *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, as well as many other bacterial species well known to one of ordinary skill in the art. Suitable bacterial expression vectors preferably comprise a promoter which functions in the host cell, one or  
25 more selectable phenotypic markers, and a bacterial origin of replication. Representative promoters include the  $\beta$ -lactamase (penicillinase) and lactose promoter system (see Chang et al., Nature 275:615, 1978), the trp promoter (Nichols and Yanofsky, Meth in Enzymology 101:155, 1983) and the tac promoter (Russell et al., Gene 20: 231, 1982). Representative selectable markers include various antibiotic resistance markers such as  
30 the kanamycin or ampicillin resistance genes. Suitable expression vectors include but are not limited to bacteriophages such as lambda derivatives or plasmids such as pBR322 (see Bolivar et al., Gene 2:95, 1977), the pUC plasmids pUC18, pUC19, pUC118, pUC119 (see Messing, Meth in Enzymology 101:20-77, 1983 and Vieira and Messing, Gene 19:259-268, 1982), and pNH8A, pNH16a, pNH18a, and Bluescript M13 (Stratagene, La Jolla, Calif.).  
35 Typical fusion expression vectors which may be used are discussed above, e.g. pGEX (Amrad Corp., Melbourne, Australia), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ). Examples of inducible non-fusion expression vectors

include pTrc (Amann et al., (1988) Gene 69:301-315) and pET 11d (Studier et al., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 60-89).

5 Yeast and fungi host cells suitable for carrying out the present invention include, but are not limited to *Saccharomyces cerevisiae*, the genera *Pichia* or *Kluyveromyces* and various species of the genus *Aspergillus*. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari et al., (1987) Embo J. 6:229-234), pMFa (Kurjan and Herskowitz, (1982) Cell 30:933-943), pJRY88 (Schultz et al., (1987) Gene 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Protocols for the transformation of yeast  
10 and fungi are well known to those of ordinary skill in the art. (see Hinnen et al., PNAS USA 75:1929, 1978; Itoh et al., J. Bacteriology 153:163, 1983, and Cullen et al. (Bio/Technology 5:369, 1987).

Mammalian cells suitable for carrying out the present invention include, among others: COS (e.g., ATCC No. CRL 1650 or 1651), BHK (e.g., ATCC No. CRL 6281), CHO  
15 (ATCC No. CCL 61), HeLa (e.g., ATCC No. CCL 2), 293 (ATCC No. 1573) and NS-1 cells. Suitable expression vectors for directing expression in mammalian cells generally include a promoter (e.g., derived from viral material such as polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40), as well as other transcriptional and translational control sequences. Examples of mammalian expression vectors include pCDM8 (Seed, B.,  
20 (1987) Nature 329:840) and pMT2PC (Kaufman et al. (1987), EMBOJ. 6:187-195).

Given the teachings provided herein, promoters, terminators, and methods for introducing expression vectors of an appropriate type into plant, avian, and insect cells may also be readily accomplished. For example, within one embodiment, the proteins of the invention may be expressed from plant cells (see Sinkar et al., J. Biosci (Bangalore)  
25 11:47-58, 1987, which reviews the use of *Agrobacterium rhizogenes* vectors; see also Zambryski et al., Genetic Engineering, Principles and Methods, Hollaender and Setlow (eds.), Vol. VI, pp. 253-278, Plenum Press, New York, 1984, which describes the use of expression vectors for plant cells, including, among others, pAS2022, pAS2023, and pAS2034).

30 Insect cells suitable for carrying out the present invention include cells and cell lines from *Bombyx* or *Spodoptera* species. Baculovirus vectors available for expression of proteins in cultured insect cells (SF 9 cells) include the pAc series (Smith et al., (1983) Mol. Cell Biol. 3:2156-2165) and the pVL series (Lucklow, V.A., and Summers, M.D., (1989) Virology 170:31-39). Some baculovirus-insect cell expression systems suitable for  
35 expression of the recombinant proteins of the invention are described in PCT/US/02442.

Alternatively, the proteins of the invention may also be expressed in non-human transgenic animals such as, rats, rabbits, sheep and pigs (see Hammer et al. (Nature

315:680-683, 1985), Palmiter et al. (Science 222:809-814, 1983), Brinster et al. (Proc Natl. Acad. Sci USA 82:44384442, 1985), Palmiter and Brinster (Cell. 41:343-345, 1985) and U.S. Patent No. 4,736,866).

5 The proteins of the invention may also be prepared by chemical synthesis using techniques well known in the chemistry of proteins such as solid phase synthesis (Merrifield, 1964, J. Am. Chem. Assoc. 85:2149-2154) or synthesis in homogenous solution (Houbenweyl, 1987, Methods of Organic Chemistry, ed. E. Wansch, Vol. 15 I and II, Thieme, Stuttgart).

10 The present invention also provides proteins comprising an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence linking the A and B chains, wherein the linker sequence contains a cleavage recognition site for a retroviral protease, such as an HIV protease or an HTLV protease. Such a protein could be prepared other than by recombinant means, for example by chemical synthesis or by conjugation of A and B chains and a linker sequence isolated and purified from their  
15 natural plant, fungal or bacterial source. Such A and B chains could be prepared having the glycosylation pattern of the native ricin-like toxin.

N-terminal or C-terminal fusion proteins comprising the protein of the invention conjugated with other molecules, such as proteins may be prepared by fusing, through recombinant techniques. The resultant fusion proteins contain a protein of the invention  
20 fused to the selected protein or marker protein as described herein. The recombinant protein of the invention may also be conjugated to other proteins by known techniques. For example the proteins may be coupled using heterobifunctional thiol-containing linkers as described in WO 90/10457, N-succinimidyl-3-(2-pyridyldithio-propionate) or N-succinimidyl-5-thioacetate. Examples of proteins which may be used to prepare fusion  
25 proteins or conjugates include cell binding proteins such as immunoglobulins, hormones, growth factors, lectins, insulin, low density lipoprotein, glucagon, endorphins, transferrin, bombesin, asialoglycoprotein glutathione-S-transferase (GST), hemagglutinin (HA), and truncated myc.

#### Utility of the Nucleic Acid Molecules and Proteins of the Invention

30 The proteins of the invention may be used to specifically inhibit or destroy mammalian cancer cells or mammalian cells infected with a retrovirus. It is an advantage of the recombinant proteins of the invention that they have specificity for the infected cells without the need for a cell binding component. The ricin-like B chain of the recombinant proteins recognize galactose moieties on the cell surface and ensure that the  
35 protein is taken up by the cell and released into the cytoplasm. When the protein is released into a non-infected cell, the A chain will remain inactive bound to the B chain. However, when the protein is released into a cell infected with a retrovirus or containing

- 19 -

an HTLV or HIV protease, the retroviral protease will cleave the cleavage recognition site in the linker, releasing the toxic A chain.

5 The specificity of a recombinant protein of the invention may be tested by treating the protein with the retroviral protease, such as HIV protease or HTLV protease which is thought to be specific for the cleavage recognition site of the linker and assaying for cleavage products. Retroviral proteases such as HIV protease or HTLV protease may be isolated from infected cells or may be prepared recombinantly, for example following the procedures in Darket et al. (1988, J. Biol. Chem. 254:2307-2312). The cleavage products may be identified for example based on size, antigenicity or activity. The toxicity of the recombinant protein may be investigated by subjecting the cleavage products to an in vitro translation assay in cell lysates, for example using Brome Mosaic Virus mRNA as a template. Toxicity of the cleavage products may be determined using a ribosomal inactivation assay (Westby et al. 1992, Bioconjugate Chem. 3:377-382). The effect of the cleavage products on protein synthesis may be measured in standardized assays of in vitro translation utilizing partially defined cell free systems composed for example of a reticulocyte lysate preparation as a source of ribosomes and various essential cofactors, such as mRNA template and amino acids. Use of radiolabelled amino acids in the mixture allows quantitation of incorporation of free amino acid precursors into trichloroacetic acid precipitable proteins. Rabbit reticulocyte lysates may be conveniently used (O'Hare, FEBS Lett. 1990, 273:200-204).

20 The ability of the recombinant proteins of the invention to selectively inhibit or destroy mammalian cells infected with a retrovirus such as cancer cells associated with HTLV or cells associated with HIV may be readily tested in vitro using mammalian cell cultures infected with the retrovirus of interest, or cancer lines. The selective inhibitory effect of the recombinant proteins of the invention may be determined by demonstrating the selective inhibition of viral antigen expression in mammalian cells, or selective inhibition of cellular proliferation in cancer cells or infected cells. For example, a selective inhibitory effect may be demonstrated by the selective inhibition of viral antigen expression in HIV-infected mononuclear phagocytic lineage cells; selective inhibition of cellular proliferation as measured against protein and DNA synthesis levels in treated, noninfected T cells and; selective loss of T cell viability. For example, the below-noted culture systems may be used to test the ability of recombinant proteins having a heterologous linker sequence containing a cleavage recognition site for the HIV protease to selectively inhibit HIV infected cells. The term HIV refers to a CD4+ dependent human immunodeficiency retrovirus, such as HIV-1 and variants thereof.

35 Normal human T lymphocytes may be prepared from peripheral blood samples and cultured in vitro, as generally described in U.S. Patent No. 4,869,903. HIV infected

- 20 -

cells may also be obtained from AIDS patients. The cells may be infected in vitro with HIV derived from an AIDS patient. The toxicity of the recombinant protein for infected and non-infected cultures may then be compared. HIV-infected T cells express HIV envelope protein on the cell surface, in particular the proteins gp120 and gp41. The ability of the recombinant protein of the invention to inhibit the expression of these viral antigens may be an important indicator of the ability of the protein to inhibit viral replication. Toxicity may be measured based upon cell death or lysis, or by a reduction in the expression of HIV antigens, such as the major envelope proteins gp120 and gp41 or the HIV core protein antigen p24.

Levels of these antigens may be measured in assays using labelled antibodies having specificity for the antigens. Inhibition of viral antigen expression has been correlated with inhibition of viral replication (U.S. Patent No. 4,869,903). Similar assays may be carried out using other suitable mammalian cells which can be cultured in vitro and which are capable of maintaining retroviral replication. Examples of suitable cells include mononuclear phagocytic lineage cells. Toxicity may also be assessed based on a decrease in protein synthesis in target cells, which may be measured by known techniques, such as incorporation of labelled amino acids, such as [3H] leucine (O'Hare et al. 1990, FEBS Lett. 273:200-204). Infected cells may also be pulsed with radiolabelled thymidine and incorporation of the radioactive label into cellular DNA may be taken as a measure of cellular proliferation.

In the models of viral infection and replication for confirming the activity of the recombinant proteins of the invention, suitable mammalian cells used as hosts are those cells which can be cultured in vitro and which are capable of maintaining viral replication. Examples of suitable cells can be human T lymphocytes or mononuclear phagocytic lineage cells. Normal human T lymphocytes may be prepared from peripheral blood samples and cultured in vitro, as generally described in U.S. Patent No. 4,869,903. Virally infected cells may also be obtained from the blood of infected patients. The toxicity of the recombinant protein for infected and non-infected cultures may then be compared. The ability of the recombinant protein of the invention to inhibit the expression of these viral antigens may be an important indicator of the ability of the protein to inhibit viral replication. Levels of these antigens may be measured in assays using labelled antibodies having specificity for the antigens. Inhibition of viral antigen expression has been correlated with inhibition of viral replication (U.S. Patent No. 4,869,903).

Toxicity may also be assessed based on a decrease in protein synthesis in target cells, which may be measured by known techniques, such as incorporation of labelled amino acids, such as [3H] leucine (O'Hare et al. 1990, FEBS Lett. 273:200-204). Infected

- 21 -

cells may also be pulsed with radiolabelled thymidine and incorporation of the radioactive label into cellular DNA may be taken as a measure of cellular proliferation. In addition, toxicity may be measured based on cell viability, for example the viability of infected and non-infected cell cultures exposed to the recombinant protein may be compared. Cell viability may be assessed by known techniques, such as trypan blue exclusion assays.

Although, the specificity of the proteins of the invention for retrovirally infected cells is mediated by the specific cleavage of the cleavage recognition site of the linker, it will be appreciated that specific cell binding components may optionally be conjugated to the proteins of the invention. Such cell binding components may be expressed as fusion proteins with the proteins of the invention or the cell binding component may be physically or chemically coupled to the protein component. Examples of suitable cell binding components include antibodies to retroviral proteins, or to cancer cell proteins.

Antibodies having specificity for a cell surface protein may be prepared by conventional methods. A mammal, (e.g., a mouse, hamster, or rabbit) can be immunized with an immunogenic form of the peptide which elicits an antibody response in the mammal. Techniques for conferring immunogenicity on a peptide include conjugation to carriers or other techniques well known in the art. For example, the peptide can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassay procedures can be used with the immunogen as antigen to assess the levels of antibodies. Following immunization, antisera can be obtained and, if desired, polyclonal antibodies isolated from the sera.

To produce monoclonal antibodies, antibody producing cells (lymphocytes) can be harvested from an immunized animal and fused with myeloma cells by standard somatic cell fusion procedures thus immortalizing these cells and yielding hybridoma cells. Such techniques are well known in the art, (e.g., the hybridoma technique originally developed by Kohler and Milstein (Nature 256, 495-497 (1975)) as well as other techniques such as the human B-cell hybridoma technique (Kozbor et al., Immunol. Today 4, 72 (1983)), the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al. Monoclonal Antibodies in Cancer Therapy (1985) Allen R. Bliss, Inc., pages 77-96), and screening of combinatorial antibody libraries (Huse et al., Science 246, 1275 (1989)). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with the peptide and the monoclonal antibodies can be isolated.

The term "antibody" as used herein is intended to include fragments thereof which also specifically react with a cell surface component. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as

- 22 -

described above. For example, F(ab')<sub>2</sub> fragments can be generated by treating antibody with pepsin. The resulting F(ab')<sub>2</sub> fragment can be treated to reduce disulfide bridges to produce Fab' fragments.

Chimeric antibody derivatives, i.e., antibody molecules that combine a non-human animal variable region and a human constant region are also contemplated within the scope of the invention. Chimeric antibody molecules can include, for example, the antigen binding domain from an antibody of a mouse, rat, or other species, with human constant regions. Conventional methods may be used to make chimeric antibodies containing the immunoglobulin variable region which recognizes a cell surface antigen (See, for example, Morrison et al., Proc. Natl Acad. Sci. U.S.A. 81,6851 (1985); Takeda et al., Nature 314, 452 (1985), Cabilly et al., U.S. Patent No. 4,816,567; Boss et al., U.S. Patent No. 4,816,397; Tanaguchi et al., European Patent Publication EP171496; European Patent Publication 0173494, United Kingdom patent GB 2177096B). It is expected that chimeric antibodies would be less immunogenic in a human subject than the corresponding non-chimeric antibody.

Monoclonal or chimeric antibodies specifically reactive against cell surface components can be further humanized by producing human constant region chimeras, in which parts of the variable regions, particularly the conserved framework regions of the antigen-binding domain, are of human origin and only the hypervariable regions are of non-human origin. Such immunoglobulin molecules may be made by techniques known in the art, (e.g., Teng et al., Proc. Natl. Acad. Sci. U.S.A., 80, 7308-7312 (1983); Kozbor et al., Immunology Today, 4, 7279 (1983); Olsson et al., Meth. Enzymol., 92, 3-16 (1982)), and PCT Publication WO92/06193 or EP 0239400). Humanized antibodies can also be commercially produced (Scotgen Limited, 2 Holly Road, Twickenham, Middlesex, Great Britain.)

Specific antibodies, or antibody fragments, reactive against cell surface components may also be generated by screening expression libraries encoding immunoglobulin genes, or portions thereof, expressed in bacteria with cell surface components. For example, complete Fab fragments, VH regions and FV regions can be expressed in bacteria using phage expression libraries (See for example Ward et al., Nature 341, 544-546: (1989); Huse et al., Science 246, 1275-1281 (1989); and McCafferty et al. Nature 348, 552-554 (1990)). Alternatively, a SCID-hu mouse, for example the model developed by Genpharm, can be used to produce antibodies, or fragments thereof.

The proteins of the invention may be formulated into pharmaceutical compositions for administration to subjects in a biologically compatible form suitable for administration *in vivo*. By "biologically compatible form suitable for administration *in vivo*" is meant a form of the substance to be administered in which any toxic effects are



- 23 -

outweighed by the therapeutic effects. The substances may be administered to living organisms including humans, and animals. Administration of a therapeutically active amount of the pharmaceutical compositions of the present invention is defined as an amount effective, at dosages and for periods of time necessary to achieve the desired result. For example, a therapeutically active amount of a substance may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of antibody to elicit a desired response in the individual. Dosage regime may be adjusted to provide the optimum therapeutic response. For example, several divided doses may be administered daily or the dose may be proportionally reduced as indicated by the exigencies of the therapeutic situation.

The active substance may be administered in a convenient manner such as by injection (subcutaneous, intravenous, etc.), oral administration, inhalation, transdermal application, or rectal administration. Depending on the route of administration, the active substance may be coated in a material to protect the compound from the action of enzymes, acids and other natural conditions which may inactivate the compound.

The compositions described herein can be prepared by per se known methods for the preparation of pharmaceutically acceptable compositions which can be administered to subjects, such that an effective quantity of the active substance is combined in a mixture with a pharmaceutically acceptable vehicle. Suitable vehicles are described, for example, in Remington's Pharmaceutical Sciences (Remington's Pharmaceutical Sciences, Mack Publishing Company, Easton, Pa., USA 1985). On this basis, the compositions include, albeit not exclusively, solutions of the substances in association with one or more pharmaceutically acceptable vehicles or diluents, and contained in buffered solutions with a suitable pH and iso-osmotic with the physiological fluids.

The pharmaceutical compositions may be used in methods for treating mammals, including humans, infected with a retrovirus. It is anticipated that the compositions will be particularly useful for treating patients infected with HIV-1, HIV-2 or cancers involving retroviruses, such as human T-cell leukemias involving HTLV. The efficacy of such treatments may be monitored by assessing the health of the patient treated and by measuring the percentage of HIV positive monocytes in treated patients.

The dose of the recombinant protein to be administered will depend on a variety of factors which may be readily monitored in human subjects. Such factors include HIV antigen levels associated with HIV infected T cells or mononuclear phagocytes; HIV antigen levels in the bloodstream; reverse transcriptase activity associated with HIV-infected T cells or mononuclear phagocytes; and the ratio of viable HIV infected cells to uninfected cells. HIV antigen levels in plasma, for example, may be readily determined using an ELISA assay.

The following non-limiting examples are illustrative of the present invention:

## **EXAMPLES**

### **EXAMPLE 1**

#### **Cloning and Expression of Prepricin Variants Activated by HIV Proteases**

##### **5 Isolation of total RNA**

The prepricin gene was cloned from new foliage of the castor bean plant. Total messenger RNA was isolated according to established procedures (Maniatis et al., *Molecular Cloning: A Lab Manual* (Cold Spring Harbour Press, Cold Spring Harbour, (1989)) and cDNA generated using reverse transcriptase.

##### **10 cDNA Synthesis:**

Oligonucleotides, corresponding to the extreme 5' and 3' ends of the prepricin gene were synthesized and used to PCR amplify the gene. Using the cDNA sequence for prepricin (Lamb et al., *Eur. J. Biochem.*, 145:266-270, 1985), several oligonucleotide primers were designed to flank the start and stop codons of the prepricin open reading  
15 frame. The oligonucleotides were synthesized using an Applied Biosystems Model 392 DNA/RNA Synthesizer. First strand cDNA synthesis was primed using the oligonucleotide Ricin1729C (Table 1). Three micrograms of total RNA was used as a template for oligo Ricin1729C primed synthesis of cDNA using Superscript II Reverse Transcriptase (BRL) following the manufacturer's protocol.

##### **20 DNA Amplification and Cloning**

The first strand cDNA synthesis reaction was used as template for DNA amplification by the polymerase chain reaction (PCR). The prepricin cDNA was amplified using the upstream primer Ricin-99 and the downstream primer Ricin1729C with Vent DNA polymerase (New England Biolabs) using standard procedures (Sambrook  
25 et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (Cold Spring Harbor Laboratory Press, 1989)). Amplification was carried out in a Biometra thermal cycler (TRIO-Thermalcycler) using the following cycling parameters: denaturation 95°C for 1 min., annealing 52°C for 1 min., and extension 72°C for 2 min., (33 cycles), followed by a final extension cycle at 72°C for 10 min. The 1846bp amplified product was fractionated on  
30 an agarose gel (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (Cold Spring Harbor Laboratory Press, 1989), and the DNA purified from the gel slice using Qiaex resin (Qiagen) following the manufacturer's protocol. The purified PCR fragment encoding the prepricin cDNA was then ligated (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (Cold Spring Harbor Laboratory Press,  
35 1989)) into an Eco RV-digested pBluescript II SK plasmid (Stratagene), and used to transform competent XL1-Blue cells (Stratagene). Positive clones were confirmed by restriction digestion of purified plasmid DNA. Plasmid DNA was extracted using a

Qiaprep Spin Plasmid Miniprep Kit (Qiagen).

#### DNA Sequencing

The cloned PCR product containing the putative preproricin gene was confirmed by DNA sequencing of the entire cDNA clone (pAP-144). Sequencing was performed using an Applied Biosystems 373A Automated DNA Sequencer, and confirmed by double-stranded dideoxy sequencing by the Sanger method using the Sequenase kit (USB). The oligonucleotide primers used for sequencing were as follows: Ricin267, Ricin486, Ricin725, Ricin937, Ricin1151, Ricin1399, Ricin1627, T3 primer (5'AATTAACCCTCACTAAAGGG-3') and T7 primer (5'GTAATACGACTCACTATAGGGC-3). Sequence data was compiled and analyzed using PC Gene software package (intelligenetics). The sequences and location of oligonucleotide primers is shown in Table 1.

#### Mutagenesis of Preproricin Linker

The preproricin cDNA clone (pAP-144) was subjected to site-directed mutagenesis in order to generate a series of variants differing only in the sequence between the A and B chains (linker region). The wild-type preproricin linker region was replaced with the three linker sequences, pAP-146, pAP-147 and pAP-148 displayed in Figure 4. The linker regions of the variants encode an HIV protease cleavage recognition sequence (Slalka et al., Cell, 56:911-913, 1989). The mutagenesis and cloning strategy used to generate the linker variant pAP-146 is summarized in Figures 1A and 1B. The mutagenesis and cloning strategy used to generate the linker variant pAP-147 is summarized in Figures 2A and 2B. The mutagenesis and cloning strategy used to generate the linker variant pAP-148 is summarized in Figures 3A and 3B. The first step involved a DNA amplification using a set of mutagenic primers (HIVA1; HIVB1; HIVH1) in combination with the two flanking primers Ricin-99Eco and Ricin1729Xba. The PCR protocol and conditions used were the same as described above. PCR products from each mutagenesis reaction were gel purified then restriction digested with either Eco RI for the A-chain encoding fragment, or Xba I for the B chain encoding fragment. Restriction digested PCR fragments were gel purified and then ligated with PBluescript SK which had been digested with Eco RI and Xba I. Ligation reactions were used to transform competent XL1-Blue cells (Stratagene). Recombinant clones were identified by restriction digests of plasmid miniprep DNA and the mutant linker sequence were confirmed by DNA sequencing.

#### Subcloning Preproricin Mutants into Vector pSB2

Full length preproricin cDNA was created from clones pAP-146, pAP-147, and pAP-148, which lack the first three nucleotides of the signal sequence (Halling et al, Nucleic Acids Research, 13:8019-8033, 1985). The missing ATG (start codon) was introduced into each mutant by site-directed mutagenesis using primers Ricin-109 and

- 26 -

Ricin1729C. The DNA template for each reaction was pAP-146, pAP-147, or pAP-148, and the PCR conditions were the same as described above. PCR products were gel purified and then ligated with Sma I-digested pSB2 (see Figure 12). Recombinant clones were identified by restriction digests of plasmid miniprep DNA, and the 5' and 3' junctions confirmed by DNA sequencing. The three constructs obtained were pAP-151, pAP-159, and pAP-163, with each having the mutant linker found in pAP-146, pAP-147, and pAP-148 respectively.

#### Subcloning Preproricin Mutants into Vector pVL1393

Preproricin variants were subcloned into the baculovirus transfer vector pVL1393 (PharMingen, sequence shown in Figure 11). The subcloning strategy for the HIV-A linker variant is summarized in Figure 5. The subcloning strategy for the HIV-B linker variant is summarized in Figure 6. The subcloning strategy for the HIV-H linker variant is summarized in Figure 7. The 1315 bp Eco RI/Kpn I fragment encoding the ricin A-chain and each mutant linker was isolated from each of the variant clones in pSB2 (pAP-151, pAP-159, and pAP-163). Each of these purified fragments was ligated with a 564 bp KpnI/PstI fragment obtained from pAP-144, and with Eco RI/Pst I cleaved pVL1393. Recombinant clones were identified by restriction digests of plasmid miniprep DNA and the 5' and 3' junctions confirmed by DNA sequencing. The three constructs obtained were pAP-190, pAP-196, and pAP-197, each having the mutant linker found in pAP-146, pAP-147, and pAP-148, respectively.

#### Isolation of Recombinant Baculoviruses

Insect cells *S. frugiperda* (Sf9), and *Trichoplusia ni* (Tn368 and BTI-TN-581-4 (High Five)) were maintained on TMN-FH medium supplemented with 10% total calf serum (Summers et al., A Manual of Methods of Baculovirus Vectors and Insect Cell Culture Procedures, (Texas Agricultural Experiment Station, 1987)). Two micrograms of recombinant pVL1393 DNA (pAP-190, pAP-196, or pAP-197) was co-transfected with 0.5 microgram of BaculoGold AcNPV DNA (PharMingen) into  $2 \times 10^6$  Tn368 insect cells following the manufacturer's protocol (Gruenwald et al., Baculovirus Expression Vector System: Procedures and Methods Manual, 2nd Edition, (San Diego, CA, 1993)). On day 5 post-transfection, media were centrifuged and the supernatants tested in limiting dilution assays with Tn368 cells (Summers et al., A Manual of Methods of Baculovirus Vectors and Insect Cell Culture Procedures, (Texas Agricultural Experiment Station, 1987)). Recombinant viruses in the supernatants were then amplified by infecting Tn368 cells at a multiplicity of infection (moi) of 0.1, followed by collection of day 7 supernatants. A total of three rounds of amplification were performed for each recombinant following established procedures (Summers et al., A Manual of Methods of Baculovirus Vectors and Insect Cell Culture Procedures, (Texas Agricultural Experiment Station, 1987 and

- 27 -

Gruenwald et al., Baculovirus Expression Vector System: Procedures and Methods Manual, 2nd Edition, (San Diego, CA, 1993)).

#### Expression of Mutant Proricin

- Recombinant baculoviruses (pAP-190baculo, pAP-196baculo, and pAP-197-baculo) were used to infect  $2 \times 10^5$  Tn368 or sf9 cells of an moi of 5 in EX-CELL400 media (JRH Biosciences) with 25mM  $\alpha$ -lactose in spinner flasks. Media supernatants containing mutant proricins were collected on day 6 post-infection.

#### Purification of Mutant Proricin

- Media supernatants were ultracentrifuged at 100,000g for 1 hour. After the addition of 1 mM phenylmethylsulfonyl fluoride, the supernatants were concentrated using an Amicon 8050 Ultrafiltration Cell fitted with a Diaflo XM50 membrane. Supernatants were then dialysed extensively against 137 mM NaCl, 2.2 mM KCl, 2.6 mM  $\text{KH}_2\text{PO}_4$ , and 8.6 mM  $\text{Na}_2\text{HPO}_4$ , pH 7.4 containing 1 mM dithiothreitol (dialysis buffer). Recombinant proricin proteins were purified by affinity chromatography using lactose agarose (Sigma) as previously described for recombinant ricin-B chain (Ferrini et al., Eur. J. Biochem., 233:772-777, 1995). Fractions containing recombinant proricin were identified using SDS/PAGE, (Sambrook et al., Molecular Cloning: A Laboratory Manual, Second Edition, (Cold Spring Harbor Laboratory Press, 1989) and by Western blot analysis using anti-ricin antibodies (Sigma).

#### In Vitro HIV Protease Digestion of Proricin Variants

- Affinity -purified mutant proricin was treated with HIV protease to confirm specific cleavage in the linker region. Proricin variants were eluted from the lactose-agarose matrix in protease digestion buffer (50mM NaCl, 50mM Na-acetate, pH 5.5, 1mM dithiothreitol) containing 100mM lactose. Proricin substrate was then incubated at 37°C for 60 minutes with 400 ng/ml recombinant HIV protease (BACHEM Biosciences Inc.). The cleavage products of proricin (ricin A and B chains) were identified using SDS/PAGE (Sambrook et al., *Molecular Cloning: a Laboratory Manual*, 2nd. ed., Cold Spring Harbor Press, 1989), followed by Western blot analysis using anti-ricin antibodies (Sigma).

#### In Vitro Translation Assay

- The activity of protease-treated proricin variants was monitored using a rabbit reticulocyte lysate in a non-radioactive (Amersham, ECL system) *in vitro* translation assay. Protease-treated proricin was added to a standard 50  $\mu$ l translation reaction mix containing Brome Mosaic Virus mRNA as template (following the manufacturer's protocol). Active ricin variants inhibit the *in vitro* translation reaction by inactivating ribosomes. Therefore, in the presence of an active ricin variant, no viral proteins are synthesized.

#### EXAMPLE 2

- 28 -

**Harvesting and affinity column purification of pro-ricin variants**

Protein samples were harvested three days post transfection. The cells were removed by centrifuging the media at 1465 g for ten minutes using a SLA-1500 (Sorvall) centrifuge rotor. The supernatant was further clarified by centrifuging at 7970g for fifteen minutes.

- 5    Protease inhibitor phenylmethyl-sulfonyl fluoride (Sigma) was added to a final concentration of 1%. The samples were concentrated (five-fold) and dialyzed (four times five-fold) into dialysis buffer (1X baculo buffer (8.6 mM  $\text{Na}_2\text{HPO}_4$ , 2.6 mM  $\text{KH}_2\text{PO}_4$ , 137 mM NaCl and 2.6 mM KCl, pH 7.4) containing 2.5 mM lactose, and 0.02%  $\text{NaN}_3$ ) using a MINITAN concentrator (Millipore) with 30kDa NMWL plates. Dithiothreitol (DTT)
- 10    was then added to a final concentration of 1 mM, and the samples were centrifuged at 37000g for one hour.

- Following centrifugation, dialysis buffer containing 1 mM DTT was added to the samples to a final volume of 500 mL. The samples were degassed and applied overnight at 4°C to an ASF-sepharose affinity column (prepared according to Pharmacia protocol) in
- 15    a 10 mL chromatography column (Biorad). The column was washed with 300 mL of wash buffer (100 mM NaOAc, pH 5.2, 1mM DTT, and 0.02%  $\text{NaN}_3$ ). Elution of pro-ricin variant was performed by applying 500 mL of elution buffer (100 mM NaOAc, pH 5.2, 250 mM lactose, and 5 mM DTT). The eluate was concentrated using an Amicon 8050 concentrator (Amicon) with a YM10 176 mm membrane, utilizing argon gas to pressurize the chamber.
- 20    The samples were further concentrated and dialyzed into 1X Baculo buffer using Ultrafree-15 Biomax (Millipore) 10 kDa NMWL filter devices, which were spun in a Beckman S4180 rotor (Beckman) at 2000g. Samples were flash frozen in dry ice and stored at -20°C.

**Purification of pAP 190 by gel filtration chromatography**

- 25    In order to purify the pro-ricin variant from processed material produced during fermentation, the protein was applied to a SUPERDEX 75 (16/60) column and SUPERDEX 200 (16/60) column (Pharmacia) connected in series equilibrated with 50 mM Tris, 100mM NaCl, pH 7.5 containing 100 mM Lactose and 0.1%  $\beta$ -mercaptoethanol ( $\beta$ ME). The flow rate of the column was 0.15 mL/min and fractions were collected every 25 minutes. The UV
- 30    (280 nm) trace was used to determine the approximate location of the purified pAP 190 and thus determine the samples for Western analysis.

**Western analysis of column fractions**

- Fractions eluted from the SUPERDEX columns (Pharmacia) were analyzed for purity using standard Western blotting techniques. An aliquot of 10 $\mu$ L from each fraction
- 35    was boiled in 1X sample buffer (62.6 mM Tris-Cl, pH 6.8, 4.4%  $\beta$ ME, 2% sodium dodecyl sulfate (SDS), 5% glycerol (all from Sigma) and 0.002% bromophenol blue (Biorad)) for

- 29 -

five minutes. Denatured samples were loaded on 12% Tris-Glycine Gels (Biorad) along with 50 ng of RCA<sub>60</sub> (Sigma) and 5 µL of kaleidoscope prestained standards (Biorad). Electrophoresis was carried out for ninety minutes at 100V in 25 mM Tris-Cl, pH 8.3, 0.1% SDS, and 192 mM glycine using the BioRad Mini Protean II cells (Biorad).

5        Following electrophoresis gels were equilibrated in transfer buffer (48 mM Tris, 39 mM glycine, 0.0375% SDS, and 20% Methanol) for a few minutes. PVDF Biorad membrane was presoaked for one minute in 100% methanol and two minutes in transfer buffer. Whatman paper was soaked briefly in transfer buffer. Five pieces of Whatman paper, membrane, gel, and another five pieces of Whatman paper were arranged on the bottom  
10 cathode (anode) of the Pharmacia Novablot transfer apparatus (Pharmacia). Transfer was for one hour at constant current (2 mA/cm<sup>2</sup>).

Transfer was confirmed by checking for the appearance of the prestained standards on the membrane. Non-specific sites on the membrane were blocked by incubating the blot for thirty minutes in 1X Phosphate Buffered Saline (1X PBS; 137 mM  
15 NaCl, 2.7 mM KCl, 8 mM Na<sub>2</sub>HPO<sub>4</sub>, 1.5 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7.4) with 5% skim milk powder (Carnation). Primary antibody (Rabbit α-ricin, Sigma) was diluted 1:3000 in 1X PBS containing 0.1% Tween 20 (Sigma) and 2.5% skim milk and incubated with blot for forty five minutes on a orbital shaker (VWR). Non-specifically bound primary antibody was removed by washing the blot for ten minutes with 1X PBS containing 0.2% Tween 20. This  
20 was repeated four times. Secondary antibody donkey anti-rabbit (Amersham) was incubated with the blot under the same conditions as the primary antibody. Excess secondary antibody was washed as described above. Blots were developed with the ECL Western Blotting detection reagents according to the manufacturer's instructions. Blots were exposed to Medtec's Full Speed Blue Film (Medtee) or Amersham's ECL Hyperfilm (Amersham) for three to fifteen minutes. Film was developed in a KODAK Automatic  
25 Developer.

**Determination of lectin binding ability of pro-ricin variant**

An Immulon 2 place (VDVR) was coated with 100 µl per well of 10µg/ml of asialofetuin and left overnight at 4°C. The plate was washed with 3X 300 µL per well  
30 with ddH<sub>2</sub>O using an automated plate washer (BioRad). The plate was blocked for one hour at 37°C by adding 300 µL per well of PBS containing 1% ovalbumin. The plate was washed again as above. Pro-ricin variant pAP 190 was added to the plate in various dilutions in 1X Baculo. A standard curve of RCA<sub>60</sub> (Sigma) from 1-10 ng was also included. The plate was incubated for 1 h at 37°C. The plate was washed as above. Anti-ricin  
35 monoclonal antibody (Sigma) was diluted 1:3000 in 1X PBS containing 0.5% ovalbumin and 0.1% tween-20, added at 100 µL per well and incubated for 1 h at 37°C. The plate was

- 30 -

washed as above. Donkey-anti rabbit polyclonal antibody was diluted 1:3000 in 1X PBS containing 0.5% ovalbumin, 0.1% Tween-20, and added at 100µL per well and incubated for 1 h at 37°C. The plate was given a final wash as described above. Substrate was added to plate at 100µL per well (1 mg/ml o-phenylenediamine (Sigma), 1 µL/ml H<sub>2</sub>O<sub>2</sub>, 25 µL of stop solution (20% H<sub>2</sub>SO<sub>4</sub>) was added and the absorbance read (A490nm-A630nm) using a SPECTRA MAX 340 plate reader (Molecular Devices).

#### Determination of pAP 190 activity using the rabbit reticulocyte assay

Ricin sample were prepared for reduction.

A) RCA<sub>60</sub> = 3,500 ng/µL of RCA<sub>60</sub> + 997 µL 1xEndo buffer (25mM Tris, 25mM KCl, 5mM MgCl<sub>2</sub>, pH 7.6)

Reduction = 95 µL of 10ng/µL + 5 µL β-mercaptoethanol

B) Ricin variants

Reduction = 40 µL variant + 2 µL β-mercaptoethanol

The ricin standard and the variants were incubated for 30 minutes at room temperature.

#### Ricin - Rabbit Reticulocyte lysate reaction

The required number of 0.5 mL tubes were labelled. (2 tubes for each sample, + and - aniline). To each of the sample tubes 20 µL of 1X endo buffer was added, and 30 µL of buffer was added to the controls. To the sample tubes either 10 µL of 10ng/µL Ricin or 10µL of variant was added. Finally, 30µL of rabbit reticulocyte lysate was added to all the tubes. The samples were incubated for 30 minutes at 30°C using the thermal block. Samples were removed from the eppendorf tube and contents added into a 1.5 mL tube containing 1 mL of TRIZOL (Gibco). Samples were incubated for 15 minutes at room temperature. After the incubation, 200 µL of chloroform was added, and the sample was vortexed and spun at 12,000 g for 15 minutes at 4°C. The top aqueous layer from the samples was removed and contents added to a 1 mL tube containing 500 µL of isopropanol. Samples were incubated for 15 minutes at room temperature and then centrifuged at 12,000 for 15 minutes at 4°C. Supernatant was removed and the pellets were washed with 1 mL of 70% ethanol. Centrifugation at 12,000 g for 5 minutes at 4°C precipitated the RNA. All but approximately 20 µL of the supernatant was removed and the remaining liquid evaporated using the speed vacuum machine. The control samples (-aniline) were dissolved in 10 µL of 0.1 X E buffer (36 mM Tris, 30 mM NaH<sub>2</sub>PO<sub>4</sub>, 1 mM EDTA, pH 7.8) and stored at -70°C or on dry ice until later. Pellets from the other samples (+aniline samples) were dissolved in 20 µL of DEPC treated ddH<sub>2</sub>O. An 80 µL aliquot of 1 M aniline (distilled) with 2.8 M acetic acid was added to these RNA samples and transferred to a fresh 0.5 mL tube. The samples were incubated in the dark for 3 minutes at 60°C. RNA



- 31 -

was precipitated by adding 100  $\mu$ L of 95% ethanol and 5  $\mu$ L of 3M sodium acetate, pH 5.2 to each tube and centrifuging at 12,000 g for 30 minutes at 4°C. Pellets were washed with 1 mL 70% ethanol and centrifuged again at 12,000g for 5 minutes at 4°C to precipitate RNA. The supernatant was removed and excess liquid evaporated using the speed vacuum machine. These pellets (+ aniline samples) were dissolved in 10  $\mu$ L of 0.1 X E buffer. To all samples (+ and - aniline), 10  $\mu$ L of formamide loading dye was added. The RNA ladder (8  $\mu$ L of ladder + 8  $\mu$ L of loading dye) was also included. Samples were incubated for 2 minutes at 70°C on the thermal block. Electrophoresis was carried out on the samples using 1.2% agarose, 50% formamide gels in 0.1X E buffer + 0.2% SDS. The gel was run for 90 minutes at 75 watts. RNA was visualized by staining the gel in 1  $\mu$ g/ $\mu$ L ethidium bromide in running buffer for 45 minutes. The gel was examined on a 302 nm UV box and photographed using the gel documentation system.

#### Results:

#### 15 Protein Expression Yields

Aliquots were taken at each stop of the harvesting/purification and tested. Yields of functional ricin variant were determined by ELISA. Typical results on an 800 mL prep of infected *T. ni* cells are given below.

Aliquot	$\mu$ g pAP190
Before concentration and dialysis	648.5
After concentration and dialysis	364.4
ASF column flow through	62.1
ASF column elution	300.7

25 Yield:  $300.7/648.5 = 46.4\%$

#### Purification of pAP 190 and Western Analysis of column fractions

Partially purified pAP 190 was applied to Superdex 75 and 200 (16/60) columns connected in series in order to remove the contaminating non-specifically processed pAP 190. Eluted fractions were tested via Western analysis and the fractions containing the most pure protein were pooled, concentrated and re-applied to the column. The variant was applied a total of three times to the column. The final purified pAP 190 has less than 1% processed variant. Figure 13 shows that the purified pAP 190 is in three fractions and the processed material eluted in two separate fractions.

The purified pAP 190 was tested for susceptibility to cleavage by HIV protease and for activation of the A-chain of the pro-ricin variant, (inhibition of protein

- 32 -

synthesis). PAP 190 was incubated with and without HIV protease for a specified time period and then electrophoresed and blotted. Cleaved pAP 190 will run as two 30 kDa proteins (B is slightly larger) under reducing (SDS-PAGE) conditions. Unprocessed pAP 190, which contains the linker region, will run at 60 kDa. HIV protease was able to cleave the pAP 190 (shown in Figure 14). Lanes B and D show untreated; while lanes C and E to G show HIV protease treated pAP 190.

#### Activation of pAP 190 variant with HIV protease

Activation of HIV protease treated pAP 190, based on the method of May *et al.* (EMBO Journal. 8 301-8, 1989) was demonstrated in Figure 15. The appearance of the 390 based pair product is observed in lane B, which is the positive control, and not observed in lane C, the negative control. Lanes D-G show that there was no N-glycosidase activity in the pAP 190 variant as predicted. Lanes H-K show that processed pAP 190 possesses N-glycosidase activity as predicted.

The pAP 190 variant has been expressed in insect cells, purified to greater than 99%, and activation of the variant has been demonstrated by cleavage with HIV protease.

#### Example 3

#### Cloning and Expression of Proricin Variants Activated by HTLV

##### Isolation of total RNA:

The preproricin gene is cloned from new foliage of the castor bean plant. Total messenger RNA is isolated according to established procedures (Maniatis *et al.*, Molecular Cloning: A Lab Manual (Cold Spring Harbour Press, Cold Spring Harbour, (1989)) and cDNA generated using reverse transcriptase.

##### cDNA Synthesis:

Oligonucleotides, corresponding to the extreme 5' and 3' ends of the preproricin gene are synthesized and used to PCR amplify the gene. Using the cDNA sequence for preproricin (Lamb *et al.*, *Eur. J. Biochem.* 145:266-270 (1985)), several oligonucleotide primers are designed to flank the start and stop codons of the preproricin open reading frame. The oligonucleotides are synthesized using an Applied Biosystems Model 392 DNA/RNA Synthesizer. First strand cDNA synthesis is primed using the oligonucleotide Ricin1729C (Table 1). Three micrograms of total RNA is used as a template for oligo Ricin1729C primed synthesis of cDNA using Superscript II Reverse Transcriptase (BRL) following the manufacturer's protocol.

##### DNA Amplification and Cloning:

The first strand cDNA synthesis reaction is used as template for DNA amplification by the polymerase chain reaction (PCR). The preproricin cDNA is amplified using the upstream primer Ricin-109 and the downstream primer Ricin1729C

with Vent DNA polymerase (New England Biolabs) using standard procedures (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (Cold Spring Harbor Laboratory Press, 1989)). Amplification is carried out in a Biometra thermal cycler (TRIO-Thermalcycler) using the following cycling parameters: denaturation 95°C for 1 min., annealing 52°C for 1 min., and extension 72°C for 2 min., (33 cycles), followed by a final extension cycle at 72°C for 10 min. The 1846bp amplified product is fractionated on an agarose gel (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (Cold Spring Harbor Laboratory Press, 1989)), and the DNA purified from the gel slice using Qiaex resin (Qiagen) following the manufacturer's protocol. The purified PCR fragment encoding the preproricin cDNA is then ligated (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (Cold Spring Harbor Laboratory Press, 1989)) into an Eco RI-digested pBluescript II SK plasmid (Stratagene), and used to transform competent XL1-Blue cells (Stratagene). Positive clones are confirmed by restriction digestion of purified plasmid DNA. Plasmid DNA is extracted using a Qiaprep Spin Plasmid Miniprep Kit (Qiagen).

#### DNA Sequencing:

The cloned PCR product containing the putative preproricin gene is confirmed by DNA sequencing of the entire cDNA clone (pAP-144). Sequencing is performed using an Applied Biosystems 373A Automated DNA Sequencer, and confirmed by double-stranded dideoxy sequencing by the Sanger method using the Sequenase kit (USB). The oligonucleotide primers used for sequencing are as follows: Ricin267, Ricin486, Ricin725, Ricin937, Ricin1151, Ricin1399, Ricin1627, T3 primer (5' AATTAACCCCTCACTAAAGGG-3') and T7 primer (5'GTAATACGACTCACTATAGGGC-3'). Sequence data is compiled and analyzed using PC Gene software package (intelligenetics). The sequences and location of oligonucleotide primers is shown in Table 1.

#### Mutagenesis of Preproricin Linker:

The preproricin cDNA clone (pAP-144) is subjected to site directed mutagenesis in order to generate a series of variants differing only in the sequence between the A and B chains (linker region). The wild-type preproricin linker region is replaced with the linker sequences displayed in Figure 20. The linker regions of the variants encode a disease-specific protease cleavage recognition sequence (Slalka et al., *Cell*, 56:911-913, 1989). The mutagenesis and cloning strategy used to generate the HTLV protease-sensitive linker variants is summarized in Figures 16A, 17A, 18A and 19A.

The first step involves a DNA amplification using a set of mutagenic primers encoding for the disease-specific protease-sensitive linker in combination with the two flanking primers Ricin-109Eco and Ricin1729Xba. The PCR protocol and conditions used

- 34 -

are the same as described above. PCR products from each mutagenesis reaction are gel purified then restriction digested with either Eco RI for the A-chain encoding fragment, or Xba I for the B chain encoding fragment. Restriction digested PCR fragments are gel purified and then ligated with pBluescript SK which has been digested with Eco RI and Xba I. Ligation reactions are used to transform competent XL1-Blue cells (Stratagene). Recombinant clones are identified by restriction digests of plasmid miniprep DNA and the mutant linker sequence are confirmed by DNA sequencing.

Subcloning Preproricin Mutants into Vector pVL1393:

Preproricin variants are subcloned into the baculovirus transfer vector pVL1393 (PharMingen). The subcloning strategy for the HTLV protease-sensitive linker variants is summarized in Figures 16C, 17C, 18C, and 19C. The 1315 bp Eco RI/Kpn I fragment encoding the ricin A-chain and each mutant linker is isolated from pAP-205, pAP-207, pAP-209 or pAP-211. Each of these purified fragments is ligated with a 564 bp KpnI/PstI fragment obtained from pAP-144, and with Eco RI/Pst I cleaved pVL1393. Recombinant clones are identified by restriction digests of plasmid miniprep DNA and the 5' and 3' junctions confirmed by DNA sequencing.

Isolation of Recombinant Baculoviruses:

Insect cells *S. frugiperda* (Sf9), and *Trichoplusia ni* (Tn368 and BTI TN-581-4 (High Five)) are maintained on TMN-FH medium supplemented with 10% total calf serum (Summers et al., A Manual of Methods of Baculovirus Vectors and Insect Cell Culture Procedures, (Texas Agricultural Experiment Station, 1987)). Two micrograms of recombinant pVL1393 DNA (pAP-190, pAP-196, or pAP-197) is co-transfected with 0.5 microgram of BaculoGold AcNPV DNA (PharMingen) into  $2 \times 10^6$  Tn368 insect cells following the manufacturer's protocol (Gruenwald et al., Baculovirus Expression Vector System: Procedures and Methods Manual, 2nd Edition, (San Diego, CA, 1993)). On day 5 post-transfection, media are centrifuged and the supernatants tested in limiting dilution assays with Tn368 cells (Summers et al., A Manual of Methods of Baculovirus Vectors and Insect Cell Culture Procedures, (Texas Agricultural Experiment Station, 1987)). Recombinant viruses in the supernatants are then amplified by infecting Tn368 cells at a multiplicity of infection (moi) of 0.1, followed by collection of day 7 supernatants. A total of three rounds of amplification are performed for each recombinant following established procedures (Summers et al., A Manual of Methods of Baculovirus Vectors and Insect Cell Culture Procedures, (Texas Agricultural Experiment Station, 1987 and Gruenwald et al., Baculovirus Expression Vector System: Procedures and Methods Manual, 2nd Edition, (San Diego, CA, 1993)).

- 35 -

Expression of Mutant Proricin:

Recombinant baculoviruses (pAP-206-baculo, pAP-208-baculo, pAP-210-baculo, and pAP-212-baculo) are used to infect  $2 \times 10^5$  Tn368 or sf9 cells of an moi of 5 in EX-CELL400 media (JRH Biosciences) with 25mM  $\alpha$ -lactose in spinner flasks. Media supernatants containing mutant proricins are collected on day 6 post-infection.

Purification of Mutant Proricin:

Media supernatants are ultracentrifuged at 100,000g for 1 hour. After the addition of 1 mM phenylmethylsulfonyl fluoride, the supernatants are concentrated using an Amicon 8050 Ultrafiltration Cell fitted with a Diaflo XM50 membrane. Supernatants are then dialysed extensively against 137 mM NaCl, 2.2 mM KCl, 2.6 mM  $\text{KH}_2\text{PO}_4$ , and 8.6 mM  $\text{Na}_2\text{HPO}_4$ , pH 7.4 containing 1 mM dithiothreitol (dialysis buffer). Recombinant proricin proteins are purified by affinity chromatography using lactose agarose (Sigma) as previously described for recombinant ricin-B chain (Ferrini et al., *Eur. J. Biochem.* 233:772-777 (1995)). Fractions containing recombinant proricin are identified using SDS/PAGE, (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (Cold Spring Harbor Laboratory Press, 1989) and by Western blot analysis using anti-ricin antibodies (Sigma).

In Vitro Protease Digestion of Proricin Variants:

Affinity-purified proricin variant is treated with individual disease-specific proteases to confirm specific cleavage in the linker region. Ricin-like toxin variants are eluted from the lactose-agarose matrix in protease digestion buffer (50mM NaCl, 50mM Na-acetate, pH 5.5, 1mM dithiothreitol) containing 100mM lactose. Proricin substrate is then incubated at 37°C for 60 minutes with a disease-specific protease. The cleavage products consisting ricin A and B chains are identified using SDS/PAGE (Sambrook et al., *Molecular Cloning: a Laboratory Manual*, 2nd. ed., Cold Spring Harbor Press, 1989), followed by Western blot analysis using anti-ricin antibodies (Sigma).

HTLV proteases may be obtained from Bachem Bioscience. Cathepsin B may be obtained from Medcor or Calbiochem.

In Vitro Translation Assay:

The activity of protease-treated ricin-like toxin variants is monitored using a rabbit reticulocyte lysate in a non-radioactive (Amersham, ECL system) *in vitro* translation assay. Protease-treated proricin is added to a standard 50 ml translation reaction mix containing Brome Mosaic Virus mRNA as template (following the manufacturer's protocol). Active ricin variants inhibit the *in vitro* translation reaction by inactivating ribosomes. Therefore, in the presence of an active ricin variant, no viral proteins are synthesized.

In Vitro Yeast Protein Synthesis Assay

- 36 -

The activity of protease-treated proricin-like toxins may also be assessed by a yeast protein synthesis assay. For example, Murakami, S et al., Mol., Cel. Biol. 2:588-592, 1982, teaches a yeast protein synthesis assay to determine ricin-like toxicity which is as sensitive as mammalian cell assays.

- 5        Six five mL cultures of *Saccharomyces cerevisiae* (Y235 cells and 2 cell wall mutants) in YPD medium (10 g/L yeast extract, 20 g/L peptone) are started by inoculating 800 uL of medium with 1 colony of *Saccharomyces cerevisiae*, vortexing, then adding 100 uL of this suspension to 5 mL of medium. Cultures are grown overnight at 30°C with gentle agitation. Cells are expanded by inoculating 100 uL of YPD medium with one or more of
- 10   the 5 mL overnight cultures and are grown at 30°C with gentle agitation until a concentration of  $1 \times 10^5$  cells/mL. Cells are washed with sterile double-distilled water, centrifuged at 1,200 g for 3 minutes and concentrated 3-fold in ZSM buffer (1 M sorbitol, 10 mM Tris-Cl, pH 7.5, 50 mM dithiothreitol (DDT)). Samples are incubated with gentle shaking for 10 minutes at 30°C, centrifuged at 1,200 g for 3 minutes and resuspended in ZSM
- 15   buffer such that the cell concentration was  $1 \times 10^8$  cells/mL. Cell walls are disrupted by adding 1 mL of beta-glucuronidase (Sigma, St. Louis, MO) to the samples and incubating for 1 hour at room temperature with gentle agitation. Cells are washed 3 times with ZSM and protoplast cells resuspended in regeneration medium (0.17% yeast nitrogen base without amino acids (Difco, Detroit, Michigan), 2 Dropout + all (essential amino acids),
- 20   10 mM Tris-Cl, pH 7.5, 2% glucose, 1M sorbitol) to a final concentration of  $1 \times 10^8$  cells/mL. An activated proricin variant which has been dialysed in sterile 1X baculo buffer (0.137 M) NaCl, 2.7 mM KCl, 2.6 mM  $\text{KH}_2\text{PO}_4$  pH 7.4) is added to one half of the protoplast, while sterile 1 X baculo buffer alone is added to the other half of the protoplasts as control. Both sets of samples are incubated at room temperature with gentle agitation. At
- 25   time periods of 0, 1, 2, and 3 hours, an aliquot of each culture is removed. The cells are diluted serially from  $10^{-4}$  to  $10^{-8}$  in ZSM and plated on soft agar (1:1 ZSM:YPD, 15% agar). Simultaneously, dilutions are made from  $10^{-2}$  to  $10^{-4}$  in sterile double-distilled water and 50 uL aliquots are plated onto YPD medium with 20% agar. Plates are incubated for 2 days at 30°C after which times colonies were counted. A plot of cell count
- 30   vs. time is used to compare the ricin test culture vs. the control culture with no ricin.

The activated proricin-like toxin variant inhibits *in vitro* protein synthesis through ribosomal inactivation. The rate of cell growth of the treatment group is expected to be substantially lower than that of the control group.

#### N-Glycosidase Activity of Proricin Variants on rRNA Oligonucleotides

- 35        Ricin-like toxins inhibit ribosomal function by hydrolysing the N-glycosidic bond between the nucleotide base and the ribose at position A4319 in eukaryotic 28S ribosomal

RNA (rRNA). The ability of the activated ricin-like toxins to inhibit ribosomal RNA (rRNA) function may be examined in an *in vitro* ribonucleotide catalysis assay using a synthetic oligoribonucleotide possessing the secondary structure of the natural RNA hydrolytic cleavage domain.

5 A synthetic 32-nucleotide RNA oligomer (University of Calgary, DNA Core Services) that mimics the 28S rRNA toxin active site is used to test the N-glycosidase activity of proricin variants. The sequence of oligonucleotide and the general methodology are substantially as described in Gluck, A. and Wool I.G., *J. Mol. Biol.* 256:838-848, 1996.

10 A labelling reaction is set up to include: 50 pmol of oligonucleotide, 20 units of T4 polynucleotide kinase (PNK; Gibco-BRL, Gaithersburg, MA), 25 pmol of  $\gamma$ -<sup>32</sup>P (Amersham, Arlington, IL), 1X T4 PNK buffer in a final volume of 50  $\mu$ L. The samples are incubated for 30 minutes at 37°C and then for 20 minutes at 65°C. The labelled oligonucleotide is precipitated with 95% ethanol and dried using a thermal cycler. A  
15 second ethanol precipitation step can be repeated to remove further trace contaminants. The RNA was resuspended to a final concentration of 1 ng/ $\mu$ L in 10 mM Tris-Cl (pH 7.6) and 50 mM NaCl (5 ng of oligonucleotide is used per sample).

Activated proricin variant is reduced in 1 X baculo buffer with 1% beta-mercaptoethanol for 30 minutes at room temperature prior to use. The oligonucleotides are  
20 heated at 90°C for 1 minute in 10 mM Tris-Cl (pH 7.6), 50 mM NaCl and allowed to renature at 0°C. CaCl<sub>2</sub>, EGTA and water are added to the renatured RNA to give the following concentrations: 3 mM Tris-HCl (pH 7.6), 15 mM NaCl, 5 mM CaCl<sub>2</sub>, and 5 mM EGTA. An activated proricin variant or ricin A-chain (Sigma, St. Louis, MO) is added to each tube. The concentration of the ricin ranged from 1-10  $\mu$ M and the proricin variant 10-  
25 fold greater. The tubes are incubated at 35°C for 20 minutes and the reaction is stopped by the addition of sodium dodecylsulfate (SDS) at a final concentration of 0.5% (w/v). The oligonucleotide and 15  $\mu$ g of added carrier tRNA (yeast tRNA; Gibco-BRL Gaithersburg, MA) are precipitated with 300 mM NaCl and 2.5 volumes of 95% ethanol. The pellets are washed once with 70% ethanol and dried on a CENTRIVAP (Labconco, Kansas City, MO).  
30 The RNA is dissolved in 5  $\mu$ L of water, 25  $\mu$ L of a solution of aniline and acetic acid (1 and 2.8 mM respectively) is added and the sample is incubated for 10 minutes at 40°C. The aniline-treated RNA is precipitate with ethanol and 300 mM NaCl, washed once in 70% ethanol and dried on the CENTRIVAP. The pellets are dissolved in 10  $\mu$ L of DEPC-treated double-distilled water and 10  $\mu$ L of 2X loading dy (178 mM Tris-HCl (pH 8.3), 178  
35 mM boric acid, 5 mM EDTA, 0.05% (w/v) bromophenol blue and 14 M urea), and are electrophoresed for 3 hours at 50 watts in 10% (w/v) polyacrylamide gel containing 7 M

- 38 -

urea in 1 X TBE buffer (89 mM Tris-HCl (pH 8.3), 89 mM boric acid, 2.5 mM boric acid, 2.5 mM EDTA). Gels are exposed to KODAK full speed blue X-ray film and left at -70°C. After 2 days, film was developed in a KODAK automatic film processor.

- 5 When proricin variant activated with a disease-specific protease is added to the oligoribonucleotide, hydrolysis of the N- glycosidic bond at position 20 (depurination of adenosine) would occur and appearance of two bands on the autograph is expected. Proricin variant without pretreatment with the disease-specific protease would not cleave the RNA oligonucleotide and would result in a single band on the autoradiograph.

In Vitro Cytotoxicity Assay:

- 10 Human ovarian cancer cells (e.g. MA148) are seeded in 96-well flat-bottom plates and are exposed to ricin-like toxin variants or control medium at 37°C for 16 h. The viability of the cancer cells is determined by measuring [<sup>35</sup>S]methionine incorporation and is significantly lower in wells treated with the toxin variants than those with control medium.

15 In Vivo Tumour Growth Inhibition Assay:

Human breast cancer (e.g. MCF-7) cells are maintained in suitable medium containing 10% fetal calf serum. The cells are grown, harvested and subsequently injected subcutaneously into ovariectomized athymic nude mice. Tumour size is determined at intervals by measuring two right-angle measurements using calipers.

20 In Vivo Tumour Metastasis Assay:

- The metastasis study is performed substantially as described in Honn, K.V. et al. (Biochem. Pharmacol. 34:235-241 (1985)). Viable B16a melanoma tumour cells are prepared and injected subcutaneously into the left axillary region of syngeneic mice. The extent of tumour metastasis is measured after 4 weeks. The lungs are removed from the animals and are fixed in Bouin's solution and macroscopic pulmonary metastases are counted using a dissecting microscope. In general without therapeutic intervention, injection of 10<sup>5</sup> viable tumour cells forms approximately 40-50 pulmonary metastases.
- 25

- Having illustrated and described the principles of the invention in a preferred embodiment, it should be appreciated to those skilled in the art that the invention can be modified in arrangement and detail without departure from such principles. We claim all
- 30 modifications coming within the scope of the following claims.



- 39 -

All publications, patents and patent applications referred to herein are incorporated by reference in their entirety to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety.

- 40 -

**TABLE 1****Table 1 - Sequence and Location of Oligonucleotide Primers**

<b>Name of Primer</b>	<b>Primer Sequence<sup>†</sup></b>	<b>Corresponds to proricin nucleotide numbers (see Figures 8-10)</b>
Ricin-109	5'-GGAGATGAAACCGGGAGGAAATACTATTGTAAT-3'	27 to 59
Ricin-99Eco	5' - <u>GCGGAATT</u> CCGGGAGGAAATACTATTGTAAT - 3'	37 to 59
Ricin 267	5' - ACGGTTTATTTTAGTTGA - 3'	300 to 317
Ricin486	5' - ACTTGCTGGTAATCTGAG - 3'	519 to 536
Ricin 725	5' - AGAATAGTTGGGGGAGAC - 3'	758 to 775
Ricin937	5' - AATGCTGATGTTTGTATG - 3'	970 to 987
Ricin1151	5' - CGGGAGTCTATGTGATGA - 3'	1184 to 1201
Ricin1399	5' - GCAAATAGTGGACAAGTA - 3'	1432 to 1449
Ricin1627	5' - GGATTGGTGTAGATGTG - 3'	1660 to 1677
Ricin1729C	5' - ATAACCTTGCTGTCCTTTCA - 3'	1864 to 1846
Ricin1729C Xba	5' - <u>CGCTCTAG</u> AATACTTGCTGTCCTTTCA - 3'	1864 to 1846

<sup>†</sup> underlined sequences inserted for subcloning purposes and not included in final preproricin sequences

- 41 -

**WE CLAIM:**

1. A purified and isolated nucleic acid having a nucleotide sequence encoding an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains, wherein the linker sequence contains a cleavage recognition site for a retroviral protease.
2. The nucleic acid of claim 1 wherein the A chain is ricin A chain.
3. The nucleic acid of claim 1 wherein the B chain is ricin B chain.
4. The nucleic acid of claim 1 wherein the cleavage recognition site is the cleavage recognition site for an HIV protease.
5. The nucleic acid of claim 1 wherein the linker amino acid sequence comprises VSQNYPIVQNFN; SKARVLAEAMSN; or SIKKILFLDGIN.
6. The nucleic acid of claim 1 having the nucleotide sequence shown in Figure 8, Figure 9 or Figure 10.
7. The nucleic acid of claim 1 wherein the cleavage recognition site is the cleavage recognition site for a human T-cell leukemia virus (HTLV) protease.
8. The nucleic acid of claim 7 wherein the linker amino acid sequence comprises SAPQVLPVMHPN; SKTKVLVVQPKN; SKTKVLVVQPRN or STTQCFPILHPN.
9. A plasmid incorporating the nucleic acid of claim 1.
10. A plasmid as claimed in claim 7 having the restriction map as shown in Figure 1A, 2A, 3A, 16A, 17A or 18A.
11. A baculovirus transfer vector incorporating the nucleic acid of claim 1.
12. A baculovirus transfer vector as claimed in claim 11 having the restriction map as shown in Figure 5, 6, 7, 16C, 17C, or 18C.
13. A baculovirus transfer vector as claimed in claim 11 having the DNA sequence as shown in Figure 11.

- 42 -

14. A recombinant protein comprising an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains, wherein the linker sequence contains a cleavage recognition site for a retroviral protease.
- 5 15. The recombinant protein of claim 14 wherein the A chain is ricin A chain.
16. The recombinant protein of claim 14 wherein the B chain is ricin B chain.
17. The recombinant protein of claim 14 wherein the cleavage recognition site is the cleavage recognition site for an HIV protease.
18. The recombinant protein of claim 14 wherein the linker amino acid sequence  
10 comprises VSQNYPIVQNFN; SKARVLAEAMSN; or SIKKILFLDGIN.
19. A recombinant protein comprising an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains, wherein the linker sequence contains a cleavage recognition site for a HTLV protease
- 15 20. The recombinant protein of claim 19 wherein the linker amino acid sequence comprises SAPQVLPVMHPN; SKTKVLVVQPKN; SKTKVLVVQPRN or STTQCFPILHPN.
21. A method of inhibiting or destroying mammalian cells infected with a retrovirus having a protease, comprising the steps of preparing a recombinant protein of  
20 claim 14 wherein the linker sequence contains a cleavage recognition site for the retrovirus protease and administering the fusion protein to the cells.
22. A method as claimed in claim 21, wherein the retrovirus is HIV.
23. A method as claimed in claim 21 wherein the mammalian cells are human cells.
- 25 24. A method of treating a mammal infected with HIV, comprising the steps of preparing a recombinant protein of claim 14 and administering the protein to the

- 43 -

mammal.

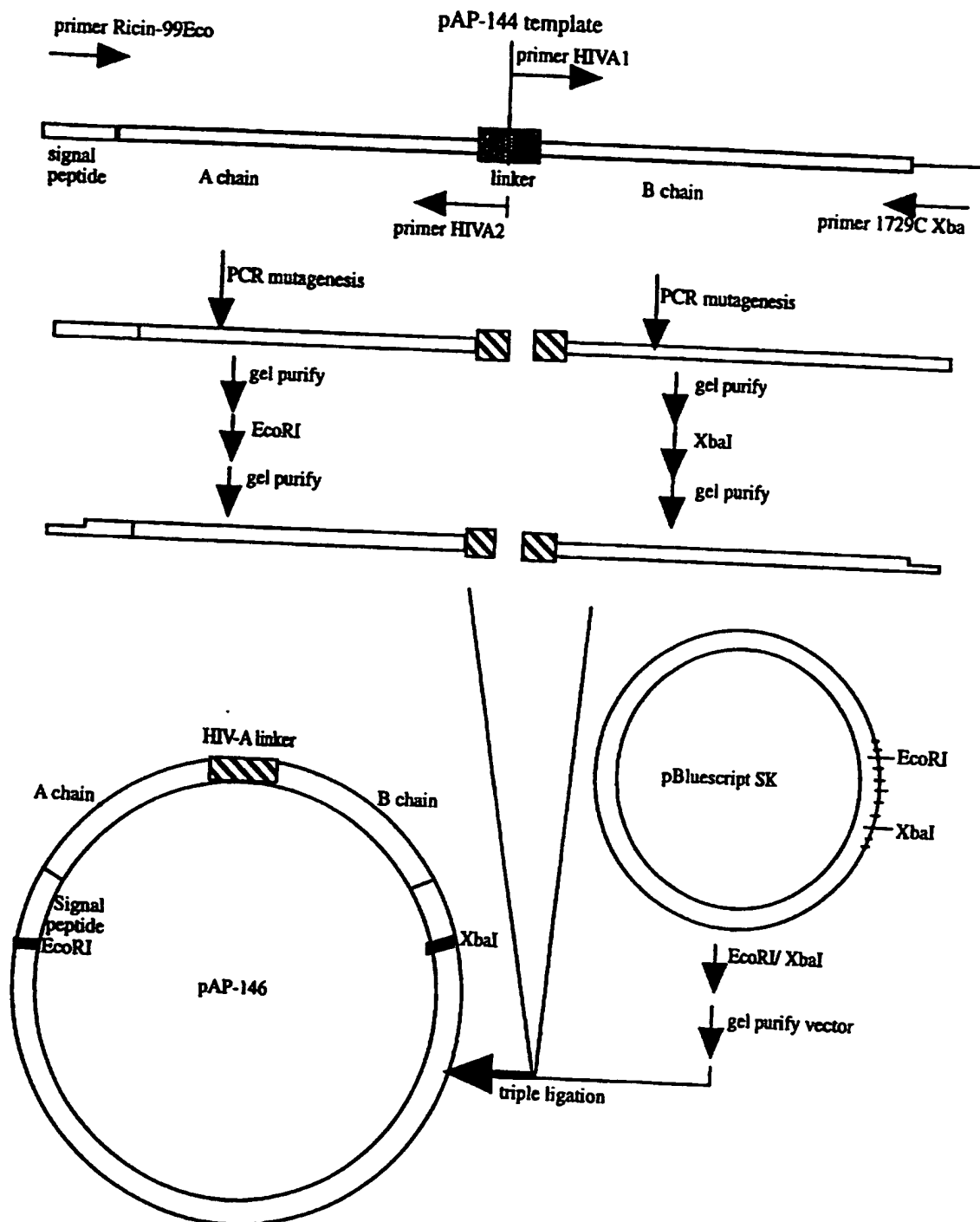
25. A process for preparing a pharmaceutical for treating a mammal infected with a retrovirus having a protease comprising the steps of preparing a purified and isolated nucleic acid having a nucleotide sequence encoding an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains, wherein the linker sequence contains a cleavage recognition site for the protease; introducing the nucleic acid into a host cell; expressing the nucleic acid in the host cell to obtain a recombinant protein comprising an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a linker amino acid sequence, linking the A and B chains wherein the linker sequence contains the cleavage recognition site for the protease, and suspending the protein in a pharmaceutically acceptable carrier, diluent or excipient.

26. A process for preparing a pharmaceutical for treating a mammal infected with a retrovirus having a protease comprising the steps of identifying a cleavage recognition site for the protease; preparing a recombinant protein comprising an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a heterologous linker amino acid sequence, linking the A and B chains, wherein the linker sequence contains the cleavage recognition site for the protease and suspending the protein in a pharmaceutically acceptable carrier, diluent or excipient.

27. A pharmaceutical composition for treating a retroviral infection in a mammal comprising the recombinant protein of claim 14 and a pharmaceutically acceptable carrier, diluent or excipient.

28. A pharmaceutical composition for treating HIV infection in a mammal comprising the recombinant protein of claim 14 and a pharmaceutically acceptable carrier, diluent or excipient.

1/47

**FIGURE 1A**

2/47

**FIGURE 1B**

WT preproreclin linker

primer HIVA1

5' - TATCCAATAGTGCAAAATTTTAATGCTGAT - 3'

TCTTTGCTTATAAGGCCAGTGGTGCCAAATTTTAAT  
 AGAAACGAATATTCGGTCACCCACGGTTTAAATTA

3' - GGTGGTAGCAGTGTCAAACAAAGCGTCTTG - 5'

primer HIVA2

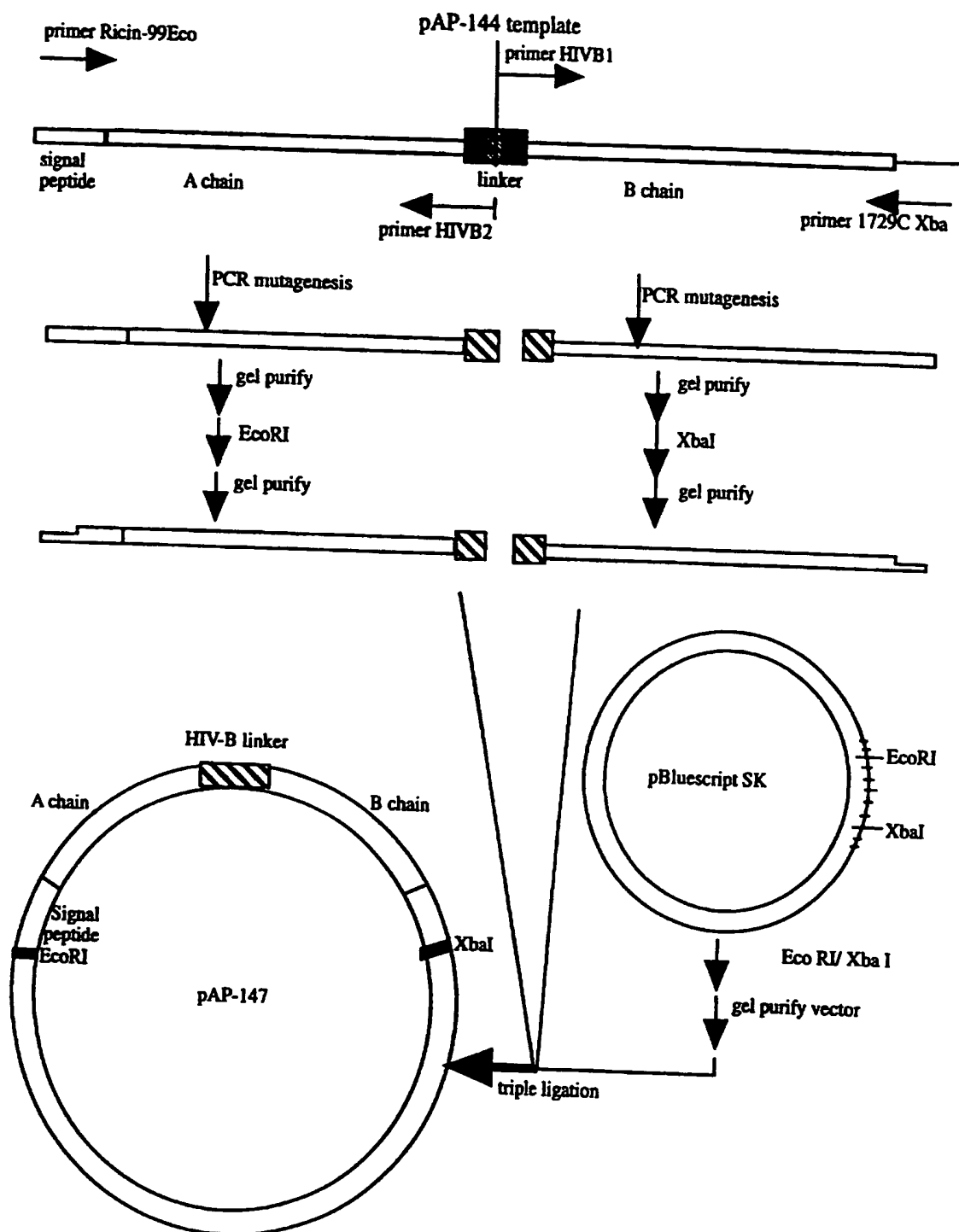
PCR mutagenesis

ligate with pBluescript SK

pAP146 linker  
(HIV-A variant)

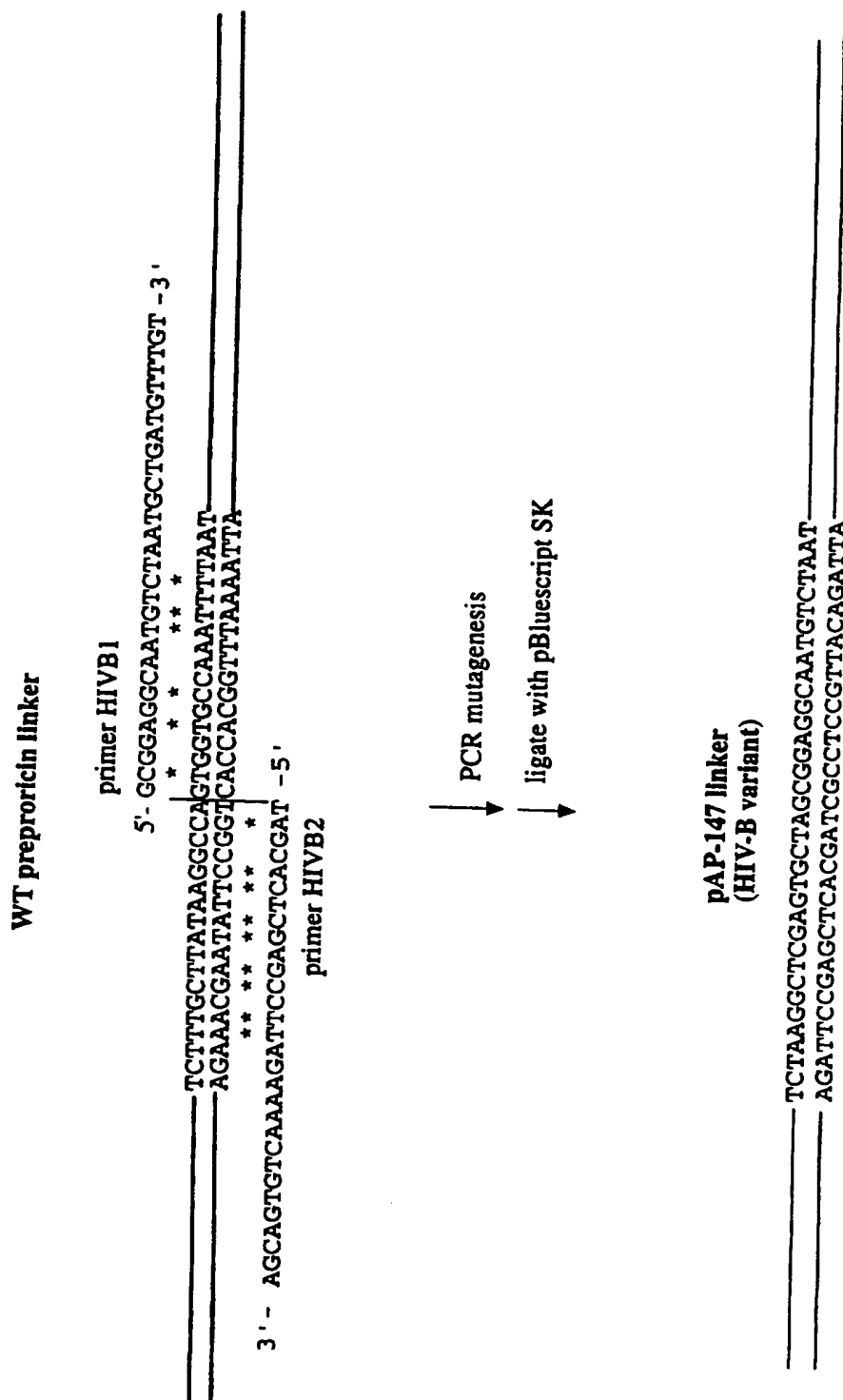
GTTTCGCAGAACTATCCAATAGTGCAAAATTTTAAT  
 CAAAGCGTCTTGATAGGTTATCACGTTTAAATTA

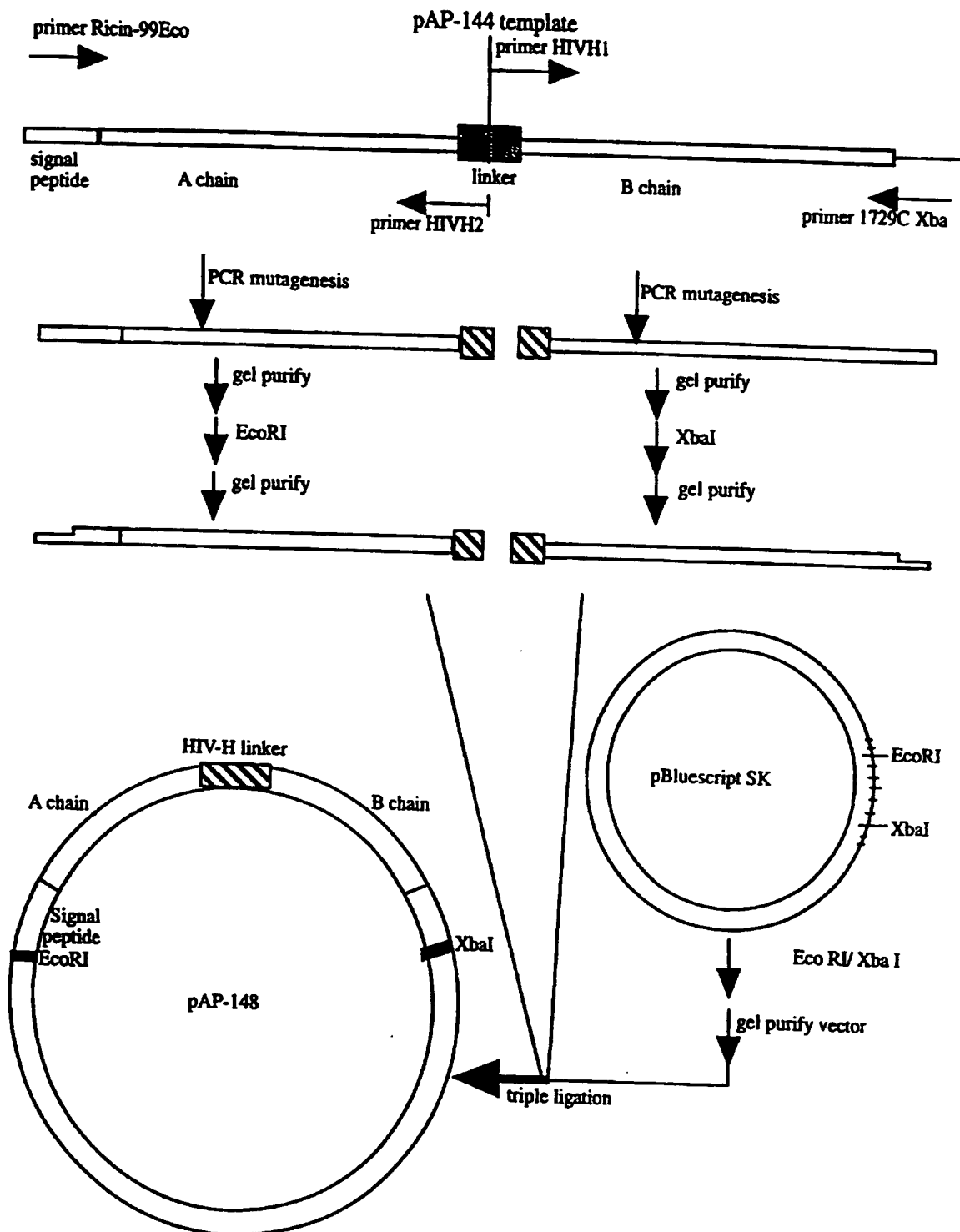
3/47

**FIGURE 2A**



4/47

**FIGURE 2B**

5/47  
**FIGURE 3A**

6/47

**FIGURE 3B**

WT preprorinclin linker

primer HIVH1

5'- TTCCTGGACGGTATTAAATGCTGATGTTTGT -3'

TCTTTGCTTATAAGGCCAGTGGTGCCAAATTTTAAT  
 AGAAACGAATATTCCGGTCACCCACGGTTTAAATTA

3'- AGCAGTGTCAAAGATAAGCATTTTAGGAT -5'

primer HIVH2

PCR mutagenesis

ligate with pBluescript SK

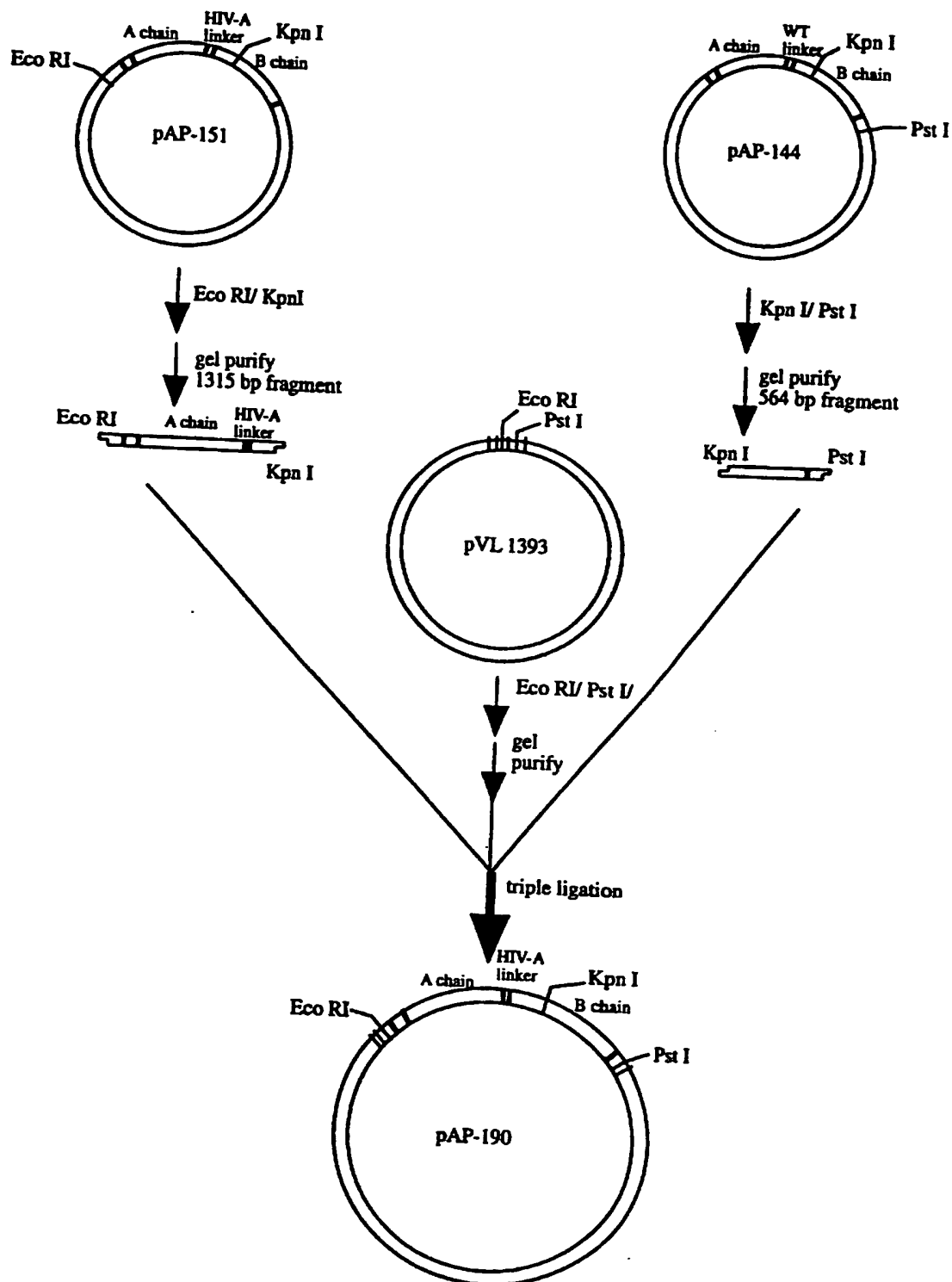
 pAP-148 linker  
 (HIV-H variant)

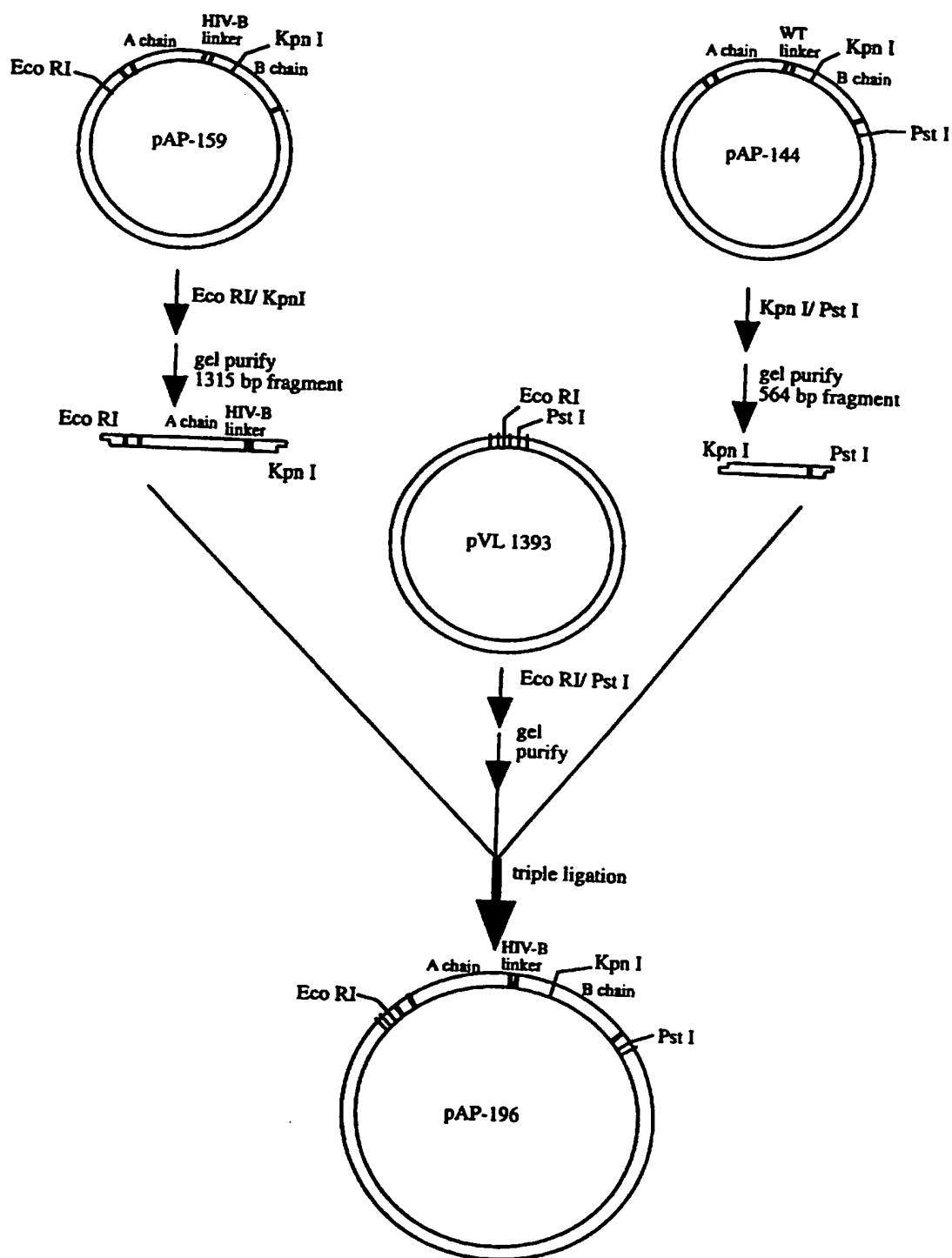
TCTATTTCGTAAATCCCTATTTCCTGGACGGTATTAAAT  
 AGATAAGCATTTTAGGATAAGGACCTGCCATAATTA

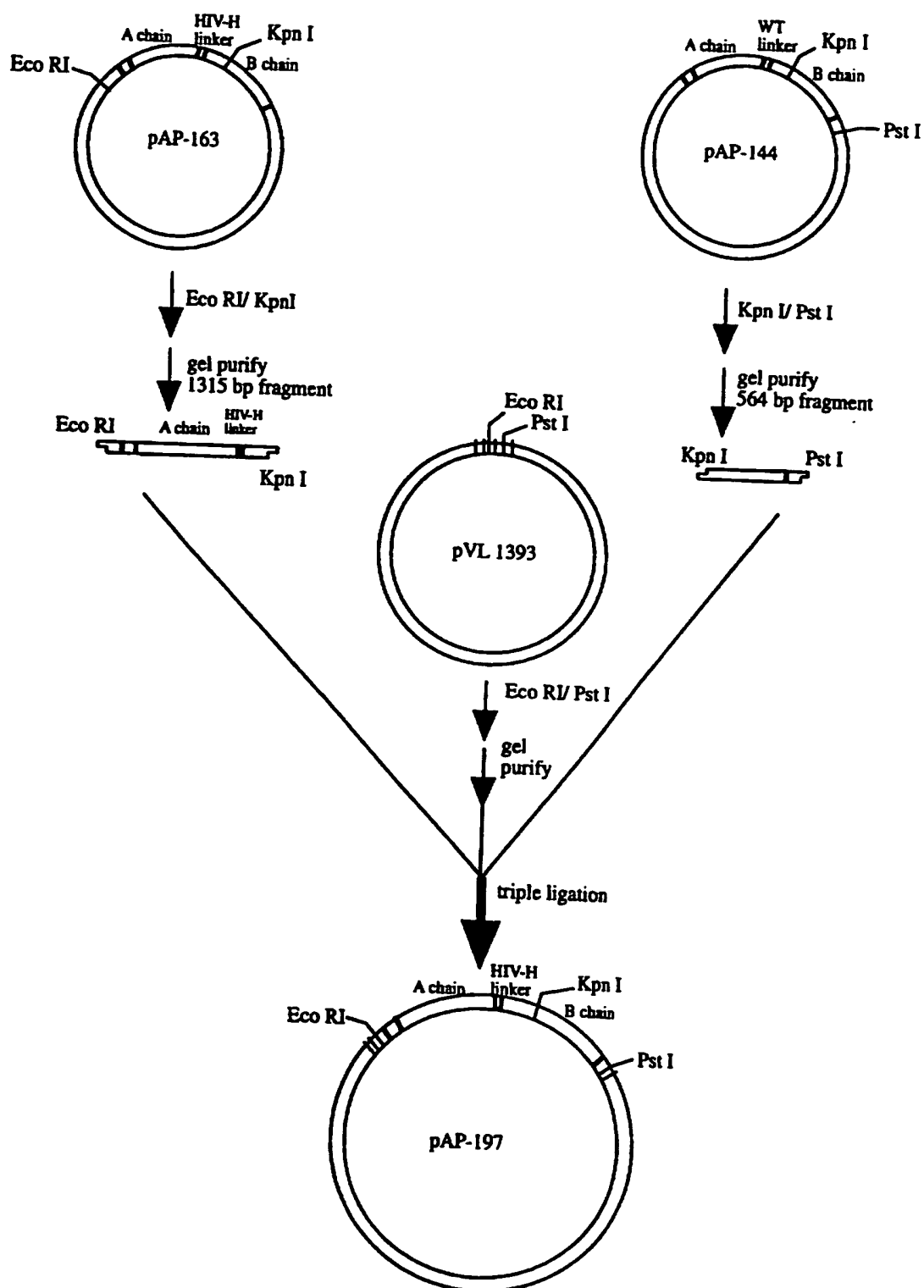
7/47  
**FIGURE 4**

Wild type Ricin linker: A chain- S L L I R P V V P N F N -B chain  
pAP-146 linker: A chain- V S Q N Y P I V Q N F N -B chain  
pAP-147 linker: A chain- S K A R V L A E A M S N -B chain  
pAP-148 linker: A chain- S I R K I L F L D G I N -B chain

pAP-146= Ricin cDNA mutant with HIV-A protease linker sequence  
pAP-147= Ricin cDNA mutant with HIV-B protease linker sequence  
pAP-148= Ricin cDNA mutant with HIV-H protease linker sequence

8/47  
**FIGURE 5**

9/47  
**FIGURE 6**

10/47  
**FIGURE 7**

11/47  
FIGURE 8

	10	20	30	40	50
1	GAATTC	CCCTCG	GAGACG	CGTCG	ACCCGG
	CTTAAG	GGGAGC	TCTGCG	CAGCTG	GGCCTCT
51	TATTGT	AATATG	GATGTAT	GCAGTG	GGCAAC
	ATAACAT	TATACCT	TACATAC	GTCAAC	CGTTGT
101	CCTCAG	GGTGGT	CTTTT	CACATT	AGAGGA
	GGAGTCC	ACCAGA	AAGTGT	AATCTCT	TATTGT
151	TACCCA	ATTATA	AACTTT	TACCAC	AGCGGT
	ATGGGT	TAAATTT	GAAATG	GTGTCG	CCACGG
201	AAACTT	TATCAG	AGCTGT	TTCGGT	CGTTT
	TTTGAA	TAGTCT	CGACA	AGCGCC	CAGCAA
251	GACATG	ATATAC	CAGTGT	TGCCAA	ACAGAG
	CTGTAC	TATATG	GTCAAC	CGTTGT	CTCAAC
301	CGGTTT	TATTTA	GTGAA	CTCTCA	AATCAT
	GCCAAAT	AAAATC	AACTTG	AGAGTT	TAGTAC
351	AGCGCT	TGGATG	TCACCA	ATGCAT	ATGTGG
	TCGCGA	CTACAG	TGGTTA	CGTATA	CACCAG
401	GCGCAT	ATTTCT	TTTCAT	CTGACA	ATCAGG
	CGCGTA	TAAAGAA	GTAGG	ACTGTT	AGTCTT
451	CATCTT	TTTCA	CTGATG	TTCAAA	TCGATA
	GTAAGAA	GTGACT	TACAAG	TTTAGC	TATATG
501	TTATGA	TAGACT	TGAACA	CTTGCT	TGGTAA
	AATACT	TATCTG	AACTTG	TGAACG	ACCATT
551	TGGGAA	TGGTCC	ACTAG	AGGAGG	CTATCT
	ACCCTT	TACCAG	GTGATC	TCTCCG	ATAGAG
601	ACTGGT	TGGCACT	CAGCTT	CCAAC	TCTGGC
	TGACC	CCGTG	AGTCG	AAGGTT	GAGACC
651	CCAAAT	GATTTT	CAGAAG	CAGCA	AAGATT
	GGTTT	ACTAA	AGTCTT	CGTCGT	TCTAAG
701	GCACGA	GAAATT	AGGTAC	AAACCG	GAGATC
	CGTGCT	CTTAAT	CCATG	TGGCCT	CTAGAC
751	ACACTT	GAGAAT	AGTTG	GGGGAG	ACTTTT
	TGTGAA	CTCTT	ATCAAC	CCCCCT	CTGAA
801	CCAAGG	AGCCTT	TGCTAG	TCCAAT	TCAACT
	GGTTC	CTCGG	AAACG	ATCAGG	TAAAGT
851	AATTC	AGTGTG	TACGAT	GTGAGT	ATATTA
	TTAAGT	CACAC	ATGTAC	ACTCAT	ATAATT
901	GTGTAT	AGATGC	GCACCT	CCACC	ATCGT
	CACATAT	CTACG	CGTGG	AGGTGG	TAGCAG



12/47  
**FIGURE 8 (Cont'd)**

951 TCCAATAGTGCAAAATTTTAAATGCTGATGTTTGTATGGATCCTGAGCCCA  
AGGTTATCACGTTTTTAAATTTACGACTACAAACATACCTAGGACTCGGGT

1001 TAGTGCCTATCGTAGGTCGAAATGGTCTATGTGTTGATGTTAGGGATGGA  
ATCACGCATAGCATCCAGCTTTACCAGATACACAACTACAATCCCTACCT

1051 AGATTCCACAACGGAACGCAATACAGTTGTGGCCATGCAAGTCTAATAC  
TCTAAGGTGTTGCCCTTTCGTTATGTCAACACCGGTACGTTTCTAGATTATG

1101 AGATGCAAAATCAGCTCTGGACTTTGAAAAGAGACAATACTATTTCGATCTA  
TCTACGTTTAGTCGAGACCTGAAACTTTTCTCTGTTATGATAAGCTAGAT

1151 ATGGAAAGTGTTTAACTACTTACGGGTACAGTCCGGGAGTCTATGTGATG  
TACCTTTTCAAAATGATGAATGCCCATGTCCAGGCCCTCAGATACACTAC

1201 ATCTATGATTGCAATACTGCTGCAACTGATGCCACCCGCTGGCAAATATG  
TAGATACTAACGTTATGACGACGTTGACTACGGTGGGCGACCGTTTATAC

1251 GGATAATGGAACCATCATAAATCCCAGATCTAGTCTAGTTTTAGCAGCGA  
CCTATTACCTTGGTAGTATTTAGGGTCTAGATCAGATCAAAATCGTCGCT

1301 CATCAGGGAACAGTGGTACCACACTTACAGTGCAAACCAACATTTATGCC  
GTAGTCCCTTGTCAACCATGGTGTGAATGTACGTTTGGTTGTAAATACGG

1351 GTTAGTCAAGGTTGGCTTCCCTACTAATAATACACAACCTTTTGTTCACAAC  
CAATCAGTTCCAACCGAAGGATGATTATTATGTGTTGGAAAACAATGTTG

1401 CATGTTGGGCTATATGGTCTGTGCTTGCAAGCAAATAGTGGACAAGTAT  
GTAACAACCCGATATACCAGACACGAACGTTCTGTTTATCACCTGTTTCATA

1451 GGATAGAGGACTGTAGCAGTGAAAAGGCTGAACAACAGTGGGCTCTTTAT  
CCTATCTCCTGACATCGTCACTTTTCCGACTTGTGTCACCCGAGAAATA

1501 GCAGATGGTTCAATACGTCCTCAGCAAAACCGAGATAATTGCCTTACAAG  
CGTCTACCAAGTTATGCAGGAGTCGTTTTGGCTCTATTAAACGGAATGTTT

1551 TGATTCTAATATACGGGAAACAGTTGTTAAGATCCTCTCTTGTGGCCCTG  
ACTAAGATTATATGCCCTTTGTCAACAATTCTAGGAGAGAACACCGGGAC

1601 CATCCTCTGGCCAACGATGGATGTTCAAGAATGATGGAACCATTTTAAAT  
GTAGGAGACCGGTGCTACCTACAAGTCTTACTACCTTGGTAAAAATTTA

1651 TTGTATAGTGGATTGGTGTAGATGTGAGGCGATCGGATCCGAGCCTTAA  
AACATATCACCTAACCAATCTACACTCCGCTAGCCTAGGCTCGGAATT

1701 ACAAATCATCTTTACCCTCTCCATGGTGACCCAAACCAATATGGTTAC  
TGTTTAGTAAGAAATGGGAGAGGTACCACTGGGTTTGGTTTATACCAATG

1751 CATTATTTTGATAGACAGATTACTCTCTTGCAAGTGTGTGTCCTGCCAT  
GTAATAAACTATCTGTCTAATGAGAGAACGTCACACACACAGGACGGTA

1801 GAAAATAGATGGCTTAAATAAAAAGGACATTGTAAATTTTGTAACTGAAA  
CTTTTATCTACCGAATTTATTTTCTGTAAACATTTAAACATTGACTTT

1851 GGACAGCAAGTTATATCGAATTCCTGCAG  
CCTGTCGTTCAATATAGCTTAAGGACGTC

13/47  
**FIGURE 9**

10 20 30 40 50

1 GAATTCCTCCCTCGAGACGCGTCGACCCGGAGATGAAACCGGGAGGAAATAC  
CTTAAGGGGAGCTCTGCGCAGCTGGGCCCTCTACTTTGGCCCTCCTTTATG

51 TATTGTAATATGGATGTATGCAGTGGCAACATGGCTTTGTTTTGGATCCA  
ATAACATTATACCTACATACGTCACCGTTGTACCGAAACAAAACCTAGGT

101 CCTCAGGGTGGTCTTTCACATTAGAGGATAACAACATATTCCCCAAACAA  
GGAGTCCCACCAGAAAGTGAATCTCCTATTGTTGTATAAGGGGTTTGT

151 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACAC  
ATGGGTAAATATTTGAAATGGTGTGCGCCACGGTGACACGTTTCGATGTG

201 AAACCTTTATCAGAGCTGTTGCGGGTCGTTTAACTGAGCTGATGTGA  
TTTGAAATAGTCTCGACAAGCGCCAGCAAATTGTTGACCTCGACTACACT

251 GACATGATATACCAGTGTGCGCAACAGAGTTGGTTTGCCCTATAAACCA  
CTGTACTATATGGTCACAACGGTTTGTCTCAACCAACGGATATTGGTT

301 CGGTTTATTTTAGTTGAACTCTCAAATCATGCAGAGCTTTCTGTTACATT  
GCCAAATAAAATCAACTTGAGAGTTTAGTACGTCGAAAGACAATGTAA

351 AGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGTGCTGGAAATA  
TCGCGACCTACAGTGGTTACGTATACACCAGCCGATGGCACGACCTTTAT

401 GCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCAGAAGCAATCACT  
CGCGTATAAAGAAAGTAGGACTGTTAGTCCTTCTACGTCTTCGTTAGTGA

451 CATCTTTTCACTGATGTTCAAAATCGATATACATTGCGCTTTGGTGGTAA  
GTAGAAAAGTGACTACAAGTTTGTAGCTATATGTAAGCGGAAACCACATT

501 TTATGATAGACTTGAACAACCTTGCTGGTAATCTGAGAGAAAATATCGAGT  
AATACTATCTGAACCTTGTGAACGACCATTTAGACTCTCTTTTATAGCTCA

551 TGGGAAATGGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGT  
ACCTTTTACCAGGTGATCTCTCCGATAGAGTCGCGAAATAATAATGTCA

601 ACTGGTGGCACTCAGCTTCCAACTCTGGCTCGTTCCTTTATAATTTGCAT  
TGACCACCGTGAGTCGAAGGTTGAGACCGAGCAAGGAAATATTAAACGTA

651 CCAAATGATTTTCAAGCAGCAAGATTCCAATATATTGAGGGAGAAATGC  
GGTTTACTAAAGTCTTCGTCGTTCTAAGGTTATATAACTCCCTCTTTACG

701 GCACGAGAATTAGGTACAACCGGAGATCTGCACCAGATCCTAGCGTAATT  
CGTGCTCTTAATCCATGTTGGCCTCTAGACGTGGTCTAGGATCGCATTA

751 ACACTTGAGAATAGTTGGGGGAGACTTTCCTGCAATTCAAGAGTCTAA  
TGTGAACCTCTTATCAACCCCTCTGAAAGGTGACGTTAAGTTCTCAGATT

801 CCAAGGAGCCTTTGCTAGTCCAATTCAACTGCAAAGACGTAATGGTTCCA  
GGTTCCTCGGAAACGATCAGGTTAAGTTGACGTTTCTGCATTACCAAGGT

851 AATTGAGTGTACGATGTGAGTATATTAATCCCTATCATAGCTCTCATG  
TTAAGTCACACATGCTACACTCATATAATTAGGGATAGTATCGAGAGTAC

901 GTGTATAGATGCGCACCTCCACCATCGTCACAGTTTCTAAGGCTCGAGT  
CACATATCTACCGTGGAGGTGGTAGCAGTGTCAAAGATTCCGAGCTCA

951 GCTAGCGGAGGCAATGTCTAATGTGATGTTTGTATGGATCCTGAGCCCA

14/47

**FIGURE 9 (Cont'd)**

CGATCGCCTCCGTTACAGATTACGACTACAAACATACCTAGGACTCGGGT

1001 TAGTGCGTATCGTAGGTCGAAATGGTCTATGTGTTGATGTTAGGGATGGA  
ATCACGCATAGCATCCAGCTTTACCAGATACACAAC TACAATCCCTACCT

1051 AGATTCCACAACGGAAACGCAATACAGTTGTGGCCATGCAAGTCTAATAC  
TCTAAGGTGTTGCCTTTGCGTTATGTCAACACCGGTACGTT CAGATTATG

1101 AGATGCAAATCAGCTCTGGACTTTGAAAAGAGACAATACTATTTCGATCTA  
TCTACGTTTAGTCGAGACCTGAAACTTTTCTCTGTTATGATAAGCTAGAT

1151 ATGGAAAGTGTTTAACTACTTACGGGTACAGTCCGGGAGTCTATGTGATG  
TACCTTTTCAAAATTGATGAATGCCATGT CAGGCCCTCAGATACACTAC

1201 ATCTATGATTGCAATACTGCTGCAACTGATGCCACCCGCTGGCAAATATG  
TAGATACTAACGTTATGACGACGTTGACTACGGTGGGCGACCGTTTATAC

1251 GGATAATGGAACCATCATAAATCCCAGATCTAGTCTAGTTTTAGCAGCGA  
CCTATTACCTTGGTAGTATTTAGGGTCTAGATCAGATCAAAATCGTCGCT

1301 CATCAGGGAACAGTGGTACCACACTTACAGTGCAAACCAACATTTATGCC  
GTAGTCCCTTGT CACCATGGTGTGAATGTCACGTTTGGTGTAAATACGG

1351 GTTAGTCAAGGTTGGCTTCCTACTAATAATACACAACCTTTTGTTACAAC  
CAATCAGTTCCAACCGAAGGATGATTATTATGTGTTGAAAACAATGTTG

1401 CATTGTTGGGCTATATGGTCTGTGCTTGCAAGCAAATAGTGGAACAAGTAT  
GTAACAACCCGATATACCAGACACGAACGTTTCGTTTATCACCTGTTTATA

1451 GGATAGAGGACTGTAGCAGTGAAAAGGCTGAACAACAGTGGGCTCTTTAT  
CCTATCTCCTGACATCGTCACTTTCCGACTTGTTGTACCCGAGAAATA

1501 GCAGATGGTTCAATACGTCCTCAGCAAAACCGAGATAATTGCCTTACAAG  
CGTCTACCAAGTTATGCAGGAGTCGTTTGGCTCTATTAAACGGAATGTTT

1551 TGATTCTAATATACGGGAAACAGTTGTTAAGATCCTCTCTTGTGGCCCTG  
ACTAAGATTATATGCCCTTTGTCAACAATTCTAGGAGAGAACACCGGGAC

1601 CATCCTCTGGCCAACGATGGATGTTCAAGAATGATGGAACCATTTTAAAT  
GTAGGAGACCGGTTGCTACCTACAAGTTCTTACTACCTTGGTAAAAATTA

1651 TTGTATAGTGGAATTGGTGTAGATGTGAGGCGATCGGATCCGAGCCTTAA  
AACATATCACCTAACCACAATCTACACTCCGCTAGCCTAGGCTCGGAATT

1701 ACAAATCATTCFTTACCCTCTCCATGGTGACCCAAACCAATATGGTTAC  
TGTTTAGTAAGAAATGGGAGAGGTACCACTGGGTTTGGTTTATACCAATG

1751 CATTATTTTGATAGACAGATTACTCTCTTGCAAGTGTGTGTCTCTGCCAT  
GTAATAAACTATCTGTCTAATGAGAGAACGTCACACACACAGGACGGTA

1801 GAAAATAGATGGCTTAAATAAAAAGGACATTGTAAATTTTGTAAGTAAAA  
CTTTTATCTACCGAATTTATTTTCTGTAAACATTTAAACATTGACTTT

1851 GGACAGCAAGTTATATCGAATTCTTCGAG  
CCTGTCGTTCAATATAGCTTAAGGACGTC

15/47  
**FIGURE 10**

10 20 30 40 50

1 GAATTCCCCTCGAGACGCGTCCGACCCGGAGATGAAACCGGGAGGAAATAC  
CTTAAGGGGAGCTCTGCGCAGCTGGGCCTCTACTTTGGCCCTCCTTTATG

51 TATTGTAATATGGATGTATGCAGTGGCAACATGGCTTTGTTTGGATCCA  
ATAACATTATACCTACATACGTCACCGTTGTACCGAAACAAAACCTAGGT

101 CCTCAGGGTGGTCTTTCACATTAGAGGATAACAACATATTTCCCAACAA  
GGAGTCCCACCAGAAAGTGTAATCTCTATTGTTGTATAAGGGGTTTGT

151 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACAC  
ATGGGTTAATATTTGAAATGGTGTGCGCCACGGTGACACGTTTCGATGTG

201 AAACCTTTATCAGAGCTGTTTCGCGGTCGTTTAACAACTGGAGCTGATGTGA  
TTTGAAATAGTCTCGACAAGCGCCAGCAAATTGTTGACCTCGACTACACT

251 GACATGATATACCAGTGTGCGCAACAGAGTTGGTTTGCCCTATAAACCAA  
CTGTACTATATGGTCACAACGGTTTGTCTCAACCAAACGGATATTTGGTT

301 CGGTTTATTTAGTTGAACCTCTCAAATCATGCAGAGCTTTCTGTTACATT  
GCCAAATAAAATCAACTTGAGAGTTTAGTACGTCTCGAAAGACAATGTAA

351 AGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGTGCTGGAAATA  
TCGCGACCTACAGTGGTTACGTATACACCAGCCGATGGCAGACCTTTAT

401 GCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCAGAAGCAATCACT  
CGCGTATAAAGAAAGTAGGACTGTTAGTCCTTCTACGCTTCGTTAGTGA

451 CATCTTTTCACTGATGTTCAAAATCGATATACATTGCGCTTTGGTGGTAA  
GTAGAAAAGTGACTACAAGTTTAGCTATATGTAAGCGGAAACCACTT

501 TTATGATAGACTTGAACAACCTTGCTGGTAACTCTGAGAGAAAATATCGAGT  
AATACTATCTGAACCTGTTGAACGACCATTAGACTCTCTTTTATAGCTCA

551 TGGGAAATGGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGT  
ACCCTTTACCAGGTGATCTCTCCGATAGAGTCGCGAAATAATAATGTCA

601 ACTGGTGGCACTCAGCTTCCAACCTCTGGCTCGTTTCTTTATAATTTGCAT  
TGACCACCGTGAGTCGAAGGTTGAGACCGAGCAAGGAAATATTAAACGTA

651 CCAAATGATTTTCAAGCAGCAAGATTCCAATATATTGAGGGAGAAATGC  
GGTTTACTAAAGTCTTCGTCTTAAGGTTATATAACTCCCTCTTTACG

701 GCACGAGAATTAGGTACAACCGGAGATCTGCACCAGATCCTAGCGTAATT  
CGTGCTCTTAATCCATGTTGGCCTCTAGACGTGGTCTAGGATCGCATTA

751 ACACCTGAGAATAGTTGGGGGAGACTTTCCACTGCAATTCAAGAGTCTAA  
TGTGAACCTCTTATCAACCCCTCTGAAAGGTGACGTTAAGTCTCAGATT

801 CCAAGGAGCCTTTGCTAGTCCAATTCAACTGCAAAGACGTAATGGTTCCA  
GGTTCTCGGAAACGATCAGGTTAAGTTGACGTTTCTGCATTACCAAGGT

851 AATTCAGTGTGTACGATGTGAGTATATTAATCCCTATCATAGCTCTCATG  
TTAAGTCACATGCTACACTCATATAATTAGGGATAGTATCGAGAGTAC

901 GTGTATAGATGCGCACCTCCACCATCGTCACAGTTTTCTATTTCGTAAT  
CACATATCTACGCGTGAGGTGGTAGCAGTGTCAAAGATAAGCATTTTA

951 CCTATTCTGGACGGTATTAATGCTGATGTTTGTATGGATCCTGAGCCCA

16/47

**FIGURE 10 (Cont'd)**

GGATAAGGACCTGCCATAATTACGACTACAAACATACCTAGGACTCGGGT

1001 TAGTGCGTATCGTAGGTCGAAATGGTCTATGTGTTGATGTTAGGGATGGA  
ATCACGCATAGCATCCAGCTTTACCAGATACACAAC TACAATCCCTACCT

1051 AGATTCCACAACGGAACGCAATACAGTTGTGGCCATGCAAGTCTAATAC  
TCTAAGGTGTTGCCCTTTGCGTTATGTCAACACCGGTACGTT CAGATTATG

1101 AGATGCAAAATCAGCTCTGGACTTTGAAAAGAGACAATACTATTTCGATCTA  
TCTACGTTTAGTCGAGACCTGAAACTTTTCTCTGTTATGATAAGCTAGAT

1151 ATGGAAAGTGTTTAACTACTTACGGGTACAGTCCGGGAGTCTATGTGATG  
TACCTTTACAAAATTGATGAATGCCCATGTCAGGCCCTCAGATACACTAC

1201 ATCTATGATTGCAATACTGCTGCAACTGATGCCACCCGCTGGCAAAATATG  
TAGATACTAACGTTATGACGACGTTGACTACGGTGGGCGACCGTTTATAC

1251 GGATAATGGAACCATCATAAATCCCAGATCTAGTCTAGTTTTAGCAGCGA  
CCTATTACCTTGGTAGTATTTAGGGTCTAGATCAGATCAAAATCGTCGCT

1301 CATCAGGGAACAGTGGTACCACACTTACAGTGCAAACCAACATTTATGCC  
GTAGTCCCTTGTCAACCATGGTGTGAATGTCACGTTTGGTTGTAATACGG

1351 GTTAGTCAAGGTTGGCTTCTACTAATAATACACAACCTTTTGTTACAAC  
CAATCAGTTCCAACCGAAGGATGATTATTATGTGTTGGAAAACAATGTTG

1401 CATTTGTTGGGTATATGGTCTGTGCTTGCAAGCAAATAGTGGACAAGTAT  
GTAACAACCCGATATACCAGACACGAACGTTTCGTTTATCACCTGTTTATA

1451 GGATAGAGGACTGTAGCAGTGAAAAGGCTGAACAACAGTGGGCTCTTTAT  
CCTATCTCTGACATCGTCACTTTTCCGACTTGTGTGTCACCCGAGAAATA

1501 GCAGATGGTTCAATACGTCCTCAGCAAAACCGAGATAATTGCCTTACAAG  
CGTCTACCAAGTTATGCAGGAGTCGTTTGGCTCTATTAAACGGAATGTTT

1551 TGATTCTAATATACGGGAAACAGTTGTTAAGATCCTCTCTTGTGGCCCTG  
ACTAAGATTATATGCCCTTTGTCAACAATTCTAGGAGAGAACACCGGGAC

1601 CATCCTCTGGCCAACGATGGATGTTCAAGAATGATGGAACCATTTTAAAT  
GTAGGAGACCGGTTGCTACCTACAAGTTCTTACTACCTTGGTAAATTTA

1651 TTGTATAGTGGATTGGTGTTAGATGTGAGGCGATCGGATCCGAGCCTTAA  
AACATATCACCTAACCACAATCTACACTCCGCTAGCCTAGGCTCGGAATT

1701 ACAAATCATTTCTTTACCCTCTCCATGGTGACCCAAACCAATATGGTTAC  
TGTTTAGTAAGAAATGGGAGAGGTACCACTGGGTTTGGTTTATACCAATG

1751 CATTATTTTGATAGACAGATTACTCTCTTGCAGTGTGTGTCTCTGCCAT  
GTAATAAACTATCTGTCTAATGAGAGAACGTCACACACAGGACGGTA

1801 GAAAATAGATGGCTTAAATAAAAAGGACATTGTAAATTTTGTAAC TGAAA  
CTTTTATCTACCGAATTTATTTTCTCTGTAACATTTAAACATTGACTTT

1851 GGACAGCAAGTTATATCGAATTCCTGCAG  
CCTGTCGTTCAATATAGCTTAAGGACGTC

17/47  
**FIGURE 11**

ID PVL1393 preliminary; circular DNA; SYN;  
9632 BP.  
XX  
AC IG1137;  
XX  
DT 01-FEB-1993 (Rel. 7, Created)  
DT 01-JUL-1995 (Rel. 12, Last updated, Version  
1)  
XX  
DE E. coli plasmid vector pVL1393 - complete.  
XX  
KW cloning vector.  
XX  
OS Cloning vector  
OC Artificial sequences; Cloning vehicles.  
XX  
RN [1]  
RC p2Bac from baculovirus  
RC p2Blue from p2Bac  
RC pBlueBac from AcNPV  
RC pBlueBac2 from AcNPV  
RC pBlueBacIII from AcNPV  
RC pBlueBacHisA from AcNPV  
RC pBlueBacHisB from AcNPV  
RC pBlueBacHisC from AcNPV  
RC pVL1392, pVL1393 from pAc360  
RA ;  
RT ;  
RL The Digest 5:2-2(1992).  
XX  
CC NM (pVL1393)  
CC CM (yes)  
CC NA (ds-DNA)  
CC TP (circular)  
CC ST ()  
CC TY (plasmid)  
CC SP (British  
Biotechnology) (Invitrogen)  
CC HO (E.coli NM522) (E.coli  
INValphaF') (insect)  
CC CP ()  
CC FN (expression) (transfer)  
CC SE ()  
CC PA (pAC360)  
CC BR (pVL1392)  
CC OF ()  
CC OR ()  
XX  
FH Key Location/Qualifiers  
FH

SUBSTITUTE SHEET (RULE 26)

18/47

**FIGURE 11 (Cont'd)**

```

FT   misc_feature           0..0
FT   polyhedrin gene        /note="1. pAc360, ori/amp/AcMNPV
FT   transposon             -> pVL1393 9632bp"
FT   transposon             0..0
FT   misc_binding           /note="TRN AcMNPV"
FT   misc_binding           868..868
FT   misc_binding           /note="SIT SacII"
FT   misc_binding           1395..1395
FT   misc_binding           /note="SIT ApaI"
FT   misc_binding           1901..1901
FT   misc_binding           /note="SIT XhoI"
FT   promoter               0..0
FT   misc_binding           /note="PRO AcMNPV polyhedrin gene"
FT   misc_binding           0..0
FT   misc_binding           /note="MCS
FT   BglIII"                BamHI-SmaI-XbaI-EcoRI-NotI-XmaIII-PstI-
FT   rep_origin              0..0
FT   pBR322)"               /note="ORI E. coli pMB1 (ColE1 and
FT   CDS                     complement(0..0)
FT   (bla)                   /note="ANT E. coli beta-lactamase gene
FT   ampicillin resistance gene (apr/amp)"
SQ   Sequence 9632 BP; 2602 A; 2122 C; 2176 G; 2732 T; 0
other;

```

```

aagctttact cgtaaagcga gttgaaggat catatttagt tgcgtttatg
agataagatt gaaagcacgt gtaaaatggt tcccgcgcgt tggcacaact
atttacaatg cggccaagtt ataaaagatt ctaatctgat atgtttttaa
acacctttgc ggcccagatt gtttgcgtac gtgactagcg aagaagatgt
gtggaccgca gaacagatag taaaacaaaa ccctagtatt ggagcaataa
tcgatttaac caacacgtct aaatattatg atggtgtgca ttttttgcgg
gcgggcctgt tatacaaaaa aattcaagta cctggccaga ctttgccgcc
tgaaagcata gttcaagaat ttattgacac ggtaaaagaa tttacagaaa
agtgtcccgg catgttggtg ggcgtgcact gcacacacgg tattaatcgc
accggttaca tgggtgtgcag atattttaatg cacaccctgg gtattgcgcc
gcaggaagcc atagatagat tcgaaaaaagc cagagggtcac aaaattgaaa
gacaaaatta cgttcaagat ttattaattt aattaatatt atttgcattc
tttaacaaat actttatcct attttcaaat tgttgcgctt cttccagcga
acaaaaacta tgcttcgctt gctccgttta gctttagacc gatcagtggc
gttggttccaa tcgacggtag gattaggccg gatattctcc accacaatgt
tggcaacggt gatgttacgt ttatgctttt ggttttccac gtacgtcttt
tggccggtaa tagccgtaaa cgtagtgcgc tcgcgcgtca cgcacaacac
cggtatgttg cgcttggtccg cgggggtattg aaccgcgcga tccgacaaat
ccaccacttt ggcaactaaa tcggtgacct gcgcgtcttt tttctgcatt
atttcgtctt tcttttgcgt ggtttcctgg aagccggtgt acatgcgggt
tagatcagtc atgacgcgcg tgacctgcaa atctttggcc tcgatctgct
tgtccttgat ggcaacgatg cgttcaataa actcttggtt ttaacaagt
tcctcggttt tttgcgccac caccgcttgc agcgcgtttg tgtgctcggt
gaatgtcgca atcagcttag tcaccaactg tttgctctcc tcctcccggt
gtttgatcgc gggatcgtag ttgccggtgc agagcacttg aggaattact
tcttctaaaa gccattcttg taattctatg gcgtaaggca atttggactt

```

SUBSTITUTE SHEET (RULE 26)

19/47

**FIGURE 11 (Cont'd)**

cataatcagc	tgaatcacgc	cggatttagt	aatgagcact	gtatgcggct
gcaaatacag	cgggtcgccc	cttttcacga	cgctgttaga	ggtagggccc
ccattttgga	tgggtctgctc	aaataacgat	ttgtatttat	tgtctacatg
aacacgtata	gctttatcac	aaactgtata	ttttaaactg	ttagcgacgt
ccttggccac	gaaccggacc	tgttggtcgc	gctctagcac	gtaccgcagg
ttgaacgtat	cttctccaaa	tttaaatctt	ccaattttta	cgcgagccat
tttgatacac	gtgtgtcgat	tttgcaacaa	ctattgtttt	ttaacgcaaa
ctaaacttat	tgtggtaagc	aataattaaa	tatgggggaa	catgcccgcg
tacaacactc	gtcgttatga	acgcagacgg	cgccggtctc	ggcgcaagcg
gctaaaacgt	gttgcgcggt	caacgcggca	aacatcgcaa	aagccaatag
tacagttttg	atttgcatat	taacggcgat	tttttaaatt	atcttattta
ataaatagtt	atgacgccta	caactccccg	cccgcgttga	ctcgtctgcac
ctcgagcagt	tcgttgacgc	cttctctcgt	gtggccgaac	acgtcgagcg
ggtggtcgat	gaccagcggc	gtgccgcacg	cgacgcacaa	gtatctgtac
accgaatgat	cgtcggggcga	aggcacgtcg	gcctccaagt	ggcaatattg
gcaaattcga	aaatatatac	agttgggttg	tttgcgcata	tctatcgtgg
cgttgggcat	gtacgtccga	acgttgattt	gcatgcaagc	cgaaattaaa
tcattgcat	tagtgcgatt	aaaacgttgt	acatcctcgc	ttttaatcat
gccgtcgatt	aaatcgcgca	atcgagtcaa	gtgatcaaag	tgtggaataa
tgttttcttt	gtattcccga	gtcaagcgca	gcgcgtattt	taacaaacta
gccatcttgt	aagttagttt	catttaatgc	aactttatcc	aataatatat
tatgtatcgc	acgtcaagaa	ttaacaatgc	gcccgttgtc	gcatctcaac
acgactatga	tagagatcaa	ataaagcgcg	aattaaatag	cttgcgacgc
aacgtgcacg	atctgtgcac	gcgttccggc	acgagctttg	attgtaataa
gtttttacga	agcgatgaca	tgacccccgt	atgacaacg	atcacgcca
aaagaactgc	cgactacaaa	attaccgagt	atgtcgggtga	cgttaaaact
attaagccat	ccaatcgacc	gttagtcgaa	tcaggaccgc	tggtgcgaga
agccgcgaag	tatggcgaat	gcacgtgata	acgtgtggag	tccgctcatt
agagcgtcat	gttttagacaa	gaaagctaca	tatttaattg	atcccgatga
ttttattgat	aaattgaccc	taactccata	cacggtattc	tacaatggcg
gggttttggg	caaaatttcc	ggactgcgat	tgtacatgct	gttaacggct
ccgcccacta	ttaatgaaat	taaaaattcc	aatttttaaaa	aacgcagcaa
gagaaacatt	tgtatgaaag	aatgcgtaga	aggaaagaaa	aatgtcgtcg
acatgctgaa	caacaagatt	aatatgcctc	cgtgtataaa	aaaaatattg
aacgatttga	aagaaaacaa	tgtaccgcgc	ggcggtatgt	acaggaagag
gtttatacta	aactgtttaca	ttgcaaacgt	ggtttcgtgt	gccaagtgtg
aaaaccgatg	tttaatcaag	gctctgacgc	atctctacaa	ccacgactcc
aagtgtgtgg	gtgaagtcat	gcatctttta	atcaaattcc	aagatgtgta
taaaccacca	aactgccaaa	aaatgaaaac	tgtcgacaag	ctctgtccgt
ttgctggcaa	ctgcaagggg	ctcaatccta	tttgtaatta	ttgaataata
aaacaattat	aaatgctaaa	tttggtttttt	attaacgata	caaaccacaa
gcaacaagaa	catttgtagt	attatctata	attgaaaacg	cgtagtataa
atcgctgagg	taatatttaa	aatcattttc	aatgattca	cagttaattt
gcgacaatat	aattttattt	tcacataaac	tagacgcctt	gtcgtcttct
tcttcgtatt	ccttctcttt	ttcatttttc	tcctcataaa	aattaacata
gttattatcg	tatccatata	tgtatctatc	gtatagagta	aattttttgt
tgtcataaat	atatatgtct	tttttaattg	gggtgtatag	accgctgcgc
atagtttttc	tgtaatttac	aacagtgcga	ttttctggta	gttcttcgga
gtgtgttgct	tttaattatta	aatttatata	atcaatgaat	ttgggatcgt
cggttttgta	caatatgttg	ccggcatagt		
acgcagcttc	ttctagtcca	attacaccat	tttttagcag	caccggatta
acataacttt	ccaaaatgtt	gtacgaaccg	ttaaacaaaa	acagttcacc
tcccttttct	atactattgt	ctgcgagcag	ttggtttgtg	ttaaaaataa
cagccattgt	aatgagacgc	acaaactaat	atcacaaact	ggaaatgtct

SUBSTITUTE SHEET (RULE 26)



20/47

**FIGURE 11 (Cont'd)**

ctgtcccgat	ttatttgaaa	cactacaaat	taaaggcgag	ctttcgtagc
aacttggttag	caatattatt	agacagctgt	gtgaagcgct	caacgatttg
cacaagcaca	atttcataca	caacgacata	aaactcgaaa	atgtcttata
tttcgaagca	cttgatcgcg	tgtatgtttg	cgattacgga	ttgtgcaaac
acgaaaactc	acttagcggtg	cacgacggca	cgttggagta	tttttagtccg
gaaaaaattc	gacacacaac	tatgcacgtt	tcgtttgact	ggtacgcggc
gtgttaacat	acaagttgct	aacgtaatca	tggtcatagc	tgtttctctgt
gtgaaattgt	tatccgctca	caattccaca	caacatacga	gccggaagca
taaagtgtaa	agcctggggg	gcctaattgag	tgagctaact	cacattaatt
gcgttgcgct	cactgccgcg	tttccagtcg	ggaaacctgt	cgtgccagct
gcattaatga	atcggccaac	gcgcggggag	aggcggtttg	cgatttgggc
gctcttccgc	ttctctcgctc	actgactcgc	tgcgctcggt	cgttcggctg
cggcgagcgg	tatcagctca	ctcaaaggcg	gtaatacggg	tatccacaga
atcaggggat	aacgcaggaa	agaacatgtg	agcaaaaggc	cagcaaaagg
ccaggaaccg	taaaaaggcc	gcgttgctgg	cgtttttcca	taggctccgc
ccccctgacg	agcatcaca	aaatcgacgc	tcaagtcaga	ggtggcgaaa
cccgacagga	ctataaagat	accaggcggt	tccccctgga	agctccctcg
tgcgctctcc	tggtccgacc	ctgcccgtta	ccggatacct	gtccgccttt
ctcccttcgg	gaagcgtggc	gctttctcat	agctcacgct	gtaggtatct
cagttcgggtg	taggtcgttc	gctccaagct	gggctgtgtg	cacgaacccc
ccgttcagcc	cgaccgctgc	gccttatccg	gtaactatcg	tcttgagtcc
aaccgggtaa				
gacacgactt	atcgccactg	gcagcagcca	ctggtaacag	gatttagcaga
gcgaggtatg	taggcgggtgc	tacagagttc	ttgaagtggg	ggcctaacta
cggctacact	agaaggacag	tatttgggtat	ctgcgctctg	ctgaagccag
ttaccttcgg	aaaaagagtt	ggtagctctt	gatccggcaa	acaaaccacc
ctgggtagcg	gtgggttttt	tggttgcaag	cagcagatta	cgcgacagaaa
aaaaggatct	caagaagatc	ctttgatctt	ttctacgggg	tctgacgctc
agtggaaacga	aaactcacgt	taagggattt	tggtcatgag	attatcaaaa
aggatcttca	cctagatcct	tttaaattaa	aaatgaagtt	ttaaatcaat
ctaaagtata	tatgagtaaa	cttgggtctga	cagttaccaa	tgcttaatca
gtgaggcacc	tatctcagcg	atctgtctat	ttcgttcatc	catagttgcc
tgactccccg	tcgtgtagat	aactacgata	cgggagggct	taccatctgg
ccccagtgct	gcaatgatac	cgcgagaccc	acgctcaccg	gctccagatt
tatcagcaat	aaaccagcca	gccggaaggg	ccgagcgcag	aagtgggtcct
gcaactttat	ccgcctccat	ccagttctatt	aattgttgcc	gggaagctag
agtaagtagt	tcgccagtta	atagtttgcg	caacgttggt	gccattgcta
caggcatcgt	ggtgtcacgc	tcgtcgtttg	gtatggcttc	attcagctcc
ggttcccaac	gatcaaggcg	agttacatga	tcccccatgt	tgtgcaaaaa
agcgggttagc	tccttcgggtc	ctccgatcgt	tgtcagaagt	aagttggccg
cagtgttatc	actcatgggt	atggcagcac	tgcataattc	tcttactgtc
atgccatccg	taagatgctt	ttctgtgact	ggtgagtact	caaccaagtc
attctgagaa	tagtgtagtc	ggcgaccgag	ttgctcttgc	ccggcggtcaa
tacgggataa	taccgcgcca	catagcagaa	ctttaaaagt	gctcatcatt
ggaaaacggt	cttcggggcg	aaaactctca	aggatcttac	cgctgttgag
atccagttcg	atgtaaccca	ctcgtgcacc	caactgatct	tcagcatctt
ttactttcac	cagcgtttct	gggtgagcaa	aaacaggaag	gcaaaatgcc
gcaaaaaagg	gaataagggc	gacacggaaa	tggtgaatac	tcatactctt
cctttttcaa	tattattgaa	gcatttatca	gggttattgt	ctcatgagcg
gatacatatt	tgaatgtatt	tagaaaaata	aacaaatagg	ggttccgcgc
acatttcccc	gaaaagtgcc	acctgacgtc	taagaaacca	ttattatcat
gacattaacc	tataaaaata	ggcgtatcac	gaggcccttt	cgtctcgcg
gtttcgggtga	tgacgggtgaa	aacctctgac	acatgcagct	cccggagacg
gtcacagctt	gtctgtaagc	ggatgccggg	agcagacaag	cccgtcaggg

SUBSTITUTE SHEET (RULE 26)

21/47

**FIGURE 11 (Cont'd)**

atcaatatat	agttgctgat	atcatggaga	taattaaaat	gataaccatc
tcgcaaataa	ataagtattt	tactgttttc	gtaacagttt	tgtaataaaa
aaacctataa	atattccgga	ttattcatac	cgtcccacca	tcgggcgcg
atcccgggta	ccttctagaa	ttccggagcg	gccgctgcag	atctgaccc
ttcctgggac	ccggcaagaa	ccaaaaactc	actctcttca	aggaaatccg
taatgttaaa	cccgaacgga	tgaagcttgt	cgttggatgg	aaaggaaaag
agttctacag	ggaaacttgg	acccgcttca	tggaagacag	cttccccatt
gttaacgacc	aagaagtgat	ggatgttttc	cttgttgcca	acatgcgtcc
cactagaccc	aaccgttgtt	acaaattcct	ggcccaacac	gctctgcgtt
gcgaccccca	ctatgtacct	catgacgtga	ttaggatcgt	cgagccttca
tgggtgggca	gcaacaacga	gtaccgcatc	agcctggcta	agaagggcg
cggctgcccc	ataatgaacc	ttcactctga	gtacaccaac	tcgttcgaac
agttcatcga	tcgtgtcatc	tggggagaact	tctacaagcc	catcgtttac
atcgggtaccg	actctgctga	agaggaggaa	attctccttg	aagtttccct
ggtgttcaaa	gtaaaggagt	ttgcaccaga	cgcacctctg	ttcactggtc
cggcggtatta	aaacacgata	cattgttatt	agtacattta	ttaagcgcta
gattctgtgc	gttgttgatt	tacagacaat	tggtgtacgt	attttaataa
ttcattaaat	ttataatctt	taggggtgga	tgtagagcg	aaaatcaaat
gattttcagc	gtctttatat	ctgaatttaa	atattaaatc	ctcaatagat
ttgtaaaata	ggtttcgatt	agtttcaaac	aaggggtgtt	ttccgaacc
gatggctgga	ctatctaata	gattttcgct	caacgccaca	aaacttgcca
aatcttgtag	cagcaatcta	gctttgtcga	tattcggttg	tggtttgttt
tgtaataaag	gttcgacgtc	gttcaaaata	ttatgcgctt	ttgtatttct
ttcatcactg	tcgttagtgt	acaattgact	cgacgtaaac	acgttaaata
aagcttggac	atatttaaca	tcgggctgtg	tagctttatt	aggccgatta
tcgtcgtcgt	cccaaccctc	gtcgttagaa	gttgcttccg	aagacgattt
tgccatagcc	acacgacgcc	tattaattgt	gtcggctaac	acgtccgcga
tcaaatttgt	agttgagctt	tttggaaatta	tttctgattg	cgggctgttt
tgggcggggt	tcaatctaac	tgtgcccgat	tttaattcag	acaacacggt
agaaagcgat	ggtgcaggcg	gtggtaacat	ttcagacggc	aatctacta
atggcgggcg	tggtggagct	gatgataaat	ctaccatcgg	tggaggcgca
ggcggggctg	gcggcgagg	cggaggcgga	ggtggtggcg	gtgatgcaga
cggcggttta	ggctcaaata	tctctttagg	caacacagtc	ggcacctcaa
ctattgtact	ggtttcgggc	gccgtttttg	gtttgaccgg	tctgagacga
gtgcgatttt	tttcggttct	aatagcttcc	aacaattggt	gtctgtcgtc
taaaggtgca	gcggggtgag	gttccgctcg	cattggtgga	gcgggcgcca
attcagacat	cgatggtggt	ggtggtggtg	gaggcgctgg	aatgttaggc
acgggagaag	gtggtggcgg	cgggtgccgc	ggtataattt	gttctggttt
agtttgttcg	cgcacgattg	tgggcaccgg	cgcaggcgcc	gctggctgca
caacggaagg	tcgtctgctt	cgaggcagcg	cttgggggtg	tggcaattca
atattataat	tggaatacaa	atcgtaaaaa	tctgctataa	gcattgtaat
ttcgctatcg	tttaccgtgc	cgatatttaa	caaccgctca	atgtaagcaa
ttgtattgta	aagagattgt	ctcaagctcg	ccgcacgccg	ataacaagcc
ttttcatttt	tactacagca	ttgtagtggc	gagacacttc	gctgtcgtcg
acgtacatgt	atgctttgtt	gtcaaaaacg	tcgttggcaa	gctttaaaat
atttaaaaga	acatctctgt	tcagcaccac	tgtgttgctg	taaatggtgt
ttttgataat	ttgcgcttcc	gcagtatcga	cacgttcaaa	aaattgatgc
gcatcaattt	tggtgttcc	attattgaat	aaataagatt	gtacagattc
atatctacga	ttcgtcatgg	ccaccacaaa	tgctacgctg	caaacgctgg
tacaatttta	cgaaaactgc	aaaaacgtca	aaactcggtg	taaaataatc
aacgggcgct	ttggcaaaat	atctatttta	tcgcacaagc	ccactagcaa
attgtatttg	cagaaaacaa	tttcggcgca	caattttaac	gctgacgaaa
taaaagttca	ccagttaatg	agcgaccacc	caaattttat	aaaaatctat
tttaatcacg	gttccatcaa	caaccaagtg	atcgtgatgg	actacattga

SUBSTITUTE SHEET (RULE 26)

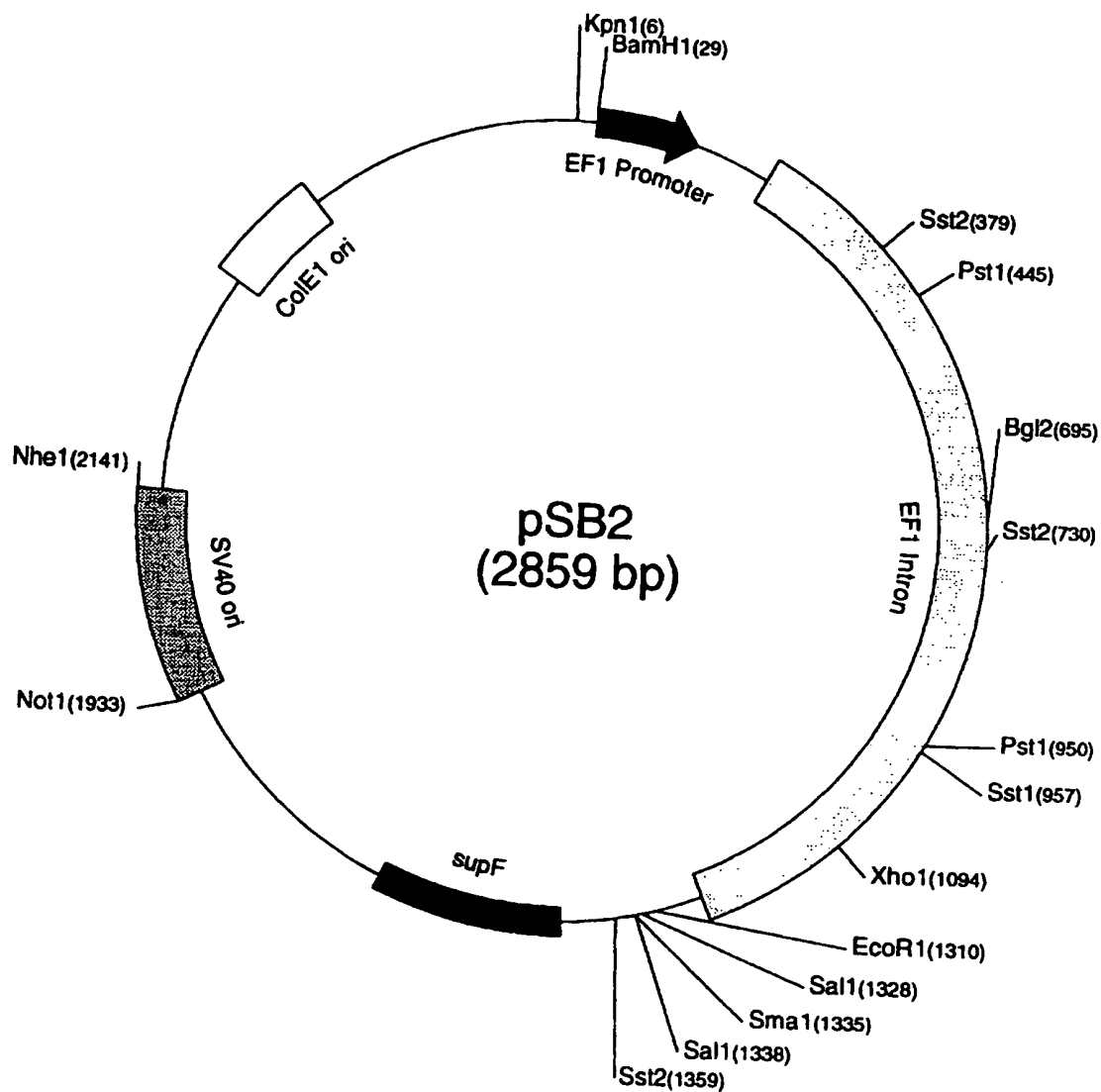
22/47

**FIGURE 11 (Cont'd)**

cgcgtcagcg ggtggttgccg ggtgtcgggg ctggcttaac tatgcggcat  
cagagcagat tgtactgaga gtgcaccata tgcggtgtga aataccgcac  
agatgcgtaa ggagaaaata ccgcatcagg cgccattcgc cattcaggct  
gcgcaactgt tgggaagggc gatcggtgcg ggcctcttcg ctattacgcc  
agctggcgaa agggggatgt gctgcaaggc gattaagttg ggtaacgcca  
gggttttccc agtcacgacg ttgtaaaacg acggccagtg cc

//

23/47

**FIGURE 12**

24/47

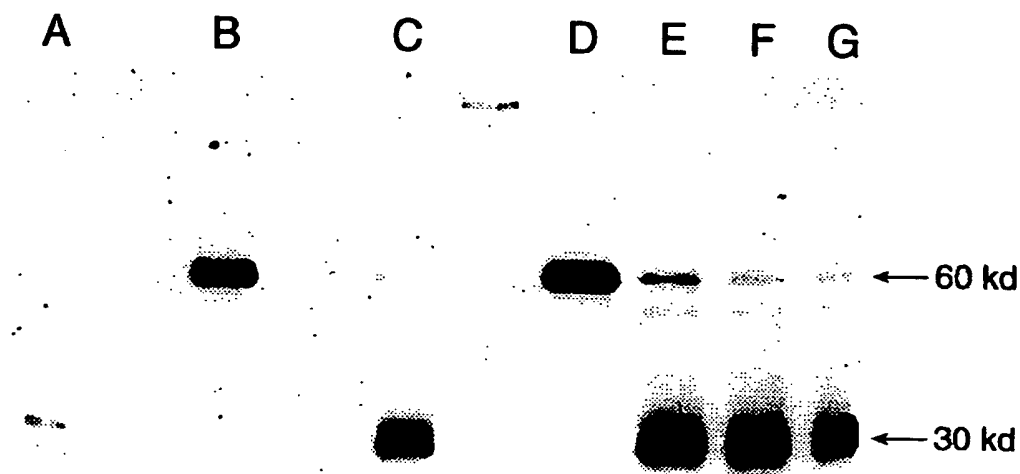
**FIGURE 13**

Confirmation of pAP 190 purity by  
Western analysis



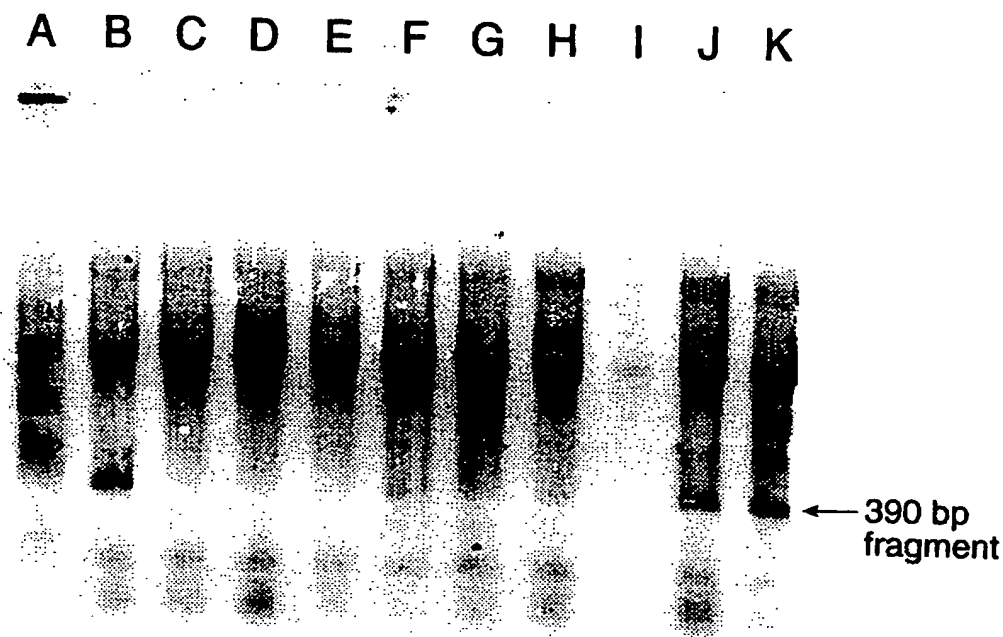
A. Ricin standard

25/47

**FIGURE 14****Cleavage of pAP 190 by HIV protease**

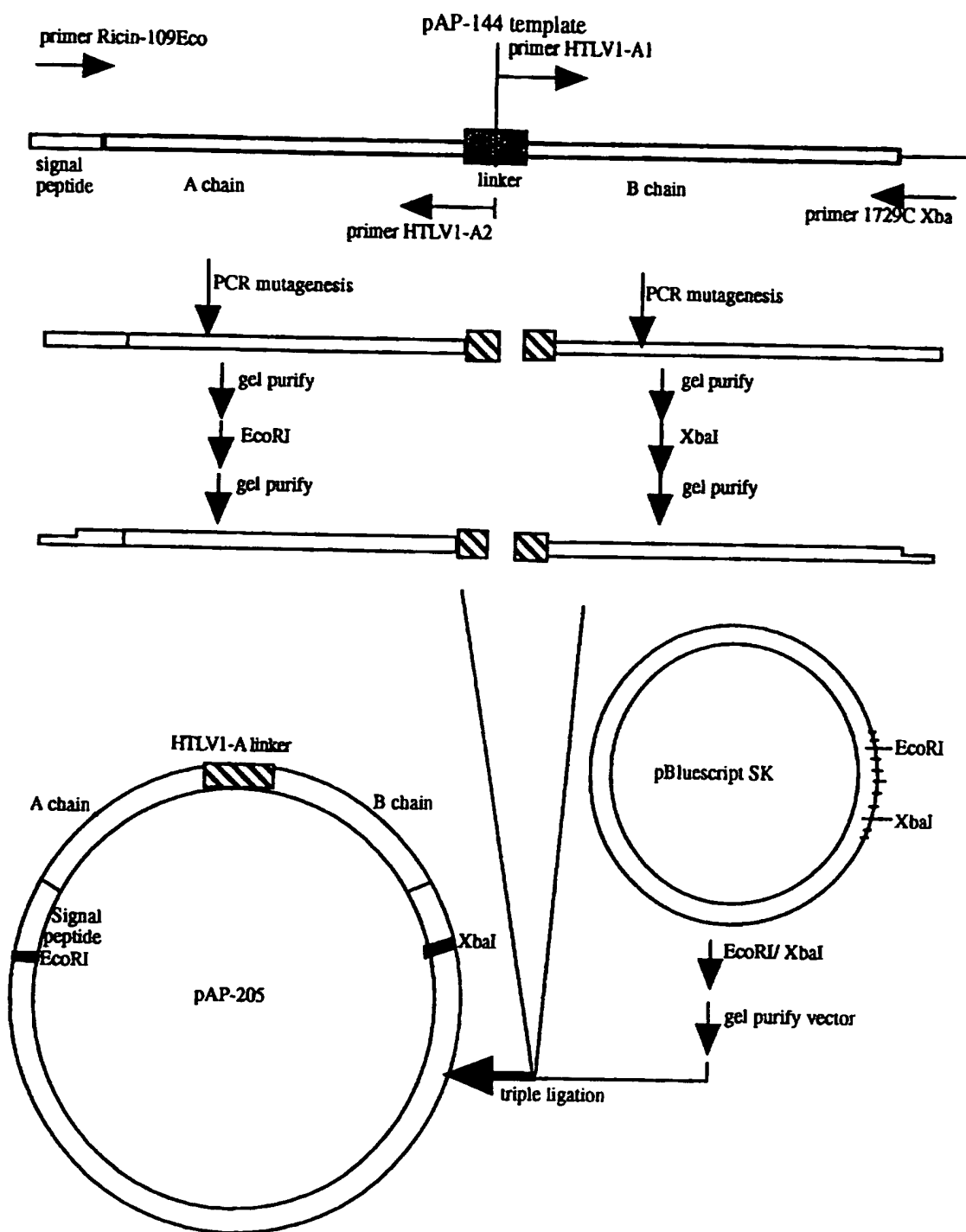
- A. Ricin standard
- B. pAP 190
- C. pAP 190 + HIV protease (3 hours)
- D. pAP 190
- E. pAP 190 + HIV protease (30 minutes)
- F. pAP 190 + HIV protease (1 hour)
- G. pAP 190 + HIV protease (2 hours)

26/47

**FIGURE 15****Activation of pAP 190**

- A. RNA Ladder
- B. Ricin A chain
- C. Negative control
- D. 340 pg pAP 190 variant
- E. 2.1 ng pAP 190 variant
- F. 12.5 ng pAP 190 variant
- G. 75 ng pAP 190 variant
- H. 340 pg 190 + HIV protease
- I. 2.1 ng 190 + HIV protease
- J. 12.5 ng 190 + HIV protease
- K. 75 ng 190 + HIV protease

27/47

**FIGURE 16A**



28/47

**FIGURE 16B****WT preproridin linker**

primer HTLV1-A1

5'- CCGGTGATGCATCCTAATGCTGATGTTGT -3'

TCTTTGCTTATAAGGCCAGTGGTCCCAAATTTTAAT  
 AGAACGAATATTCGGT\*  
 CACCACGGTTAAATTA

3'- AGCAGTGTCAAAAGACGGGAGTTCACGAT-5'

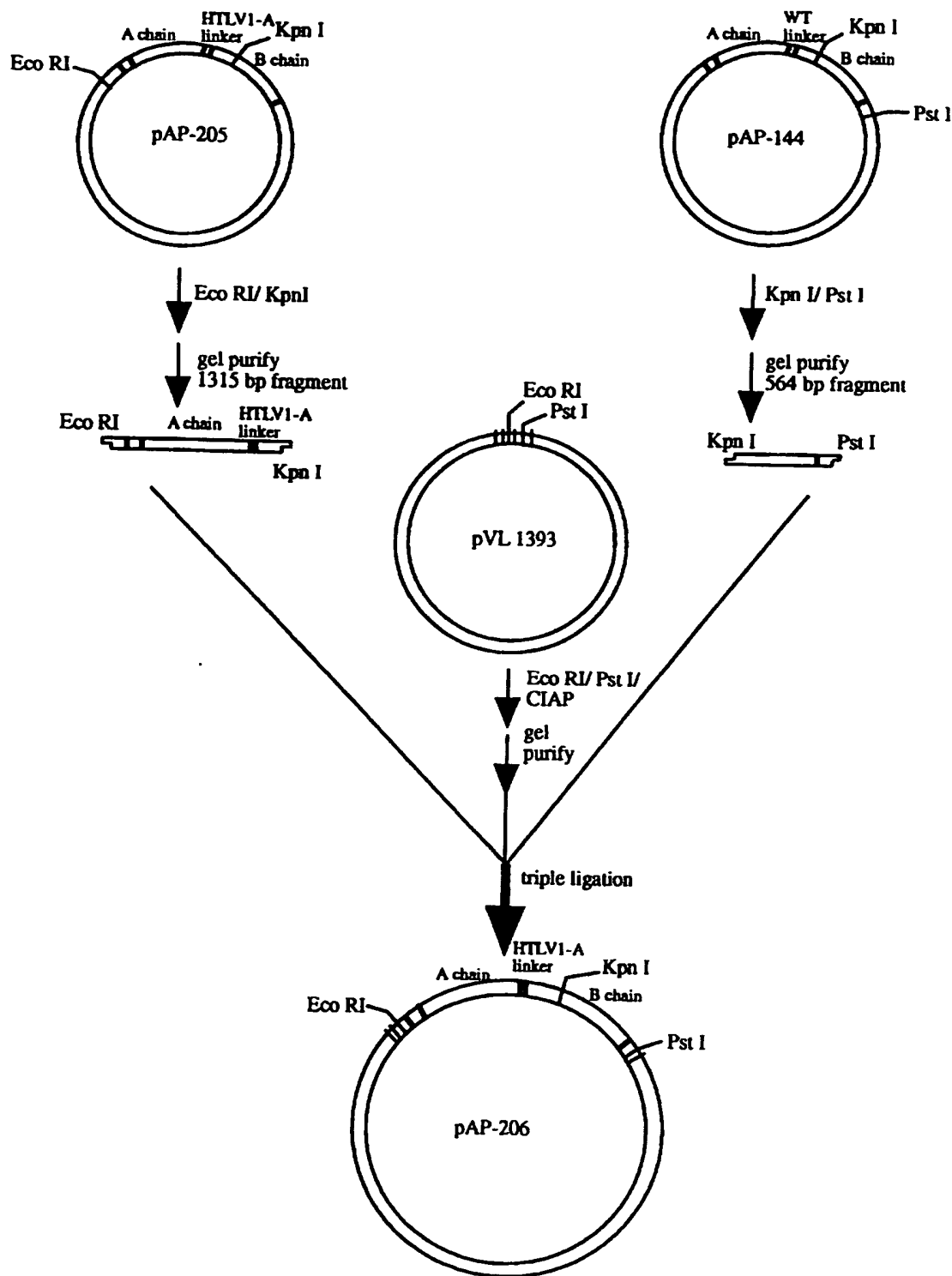
primer HTLV1-A2

PCR mutagenesis

ligate with pBluescript SK

PAP 205 linker  
 (HTLV1-A variant)

TCTGGCCTCAAGTGTACCGGTGATGCATCCTAAT  
 AGACGGGAGTTCACGATGCCACTACGTAGGATTA

29/47  
**FIGURE 16C**

30/47

FIGURE 16D

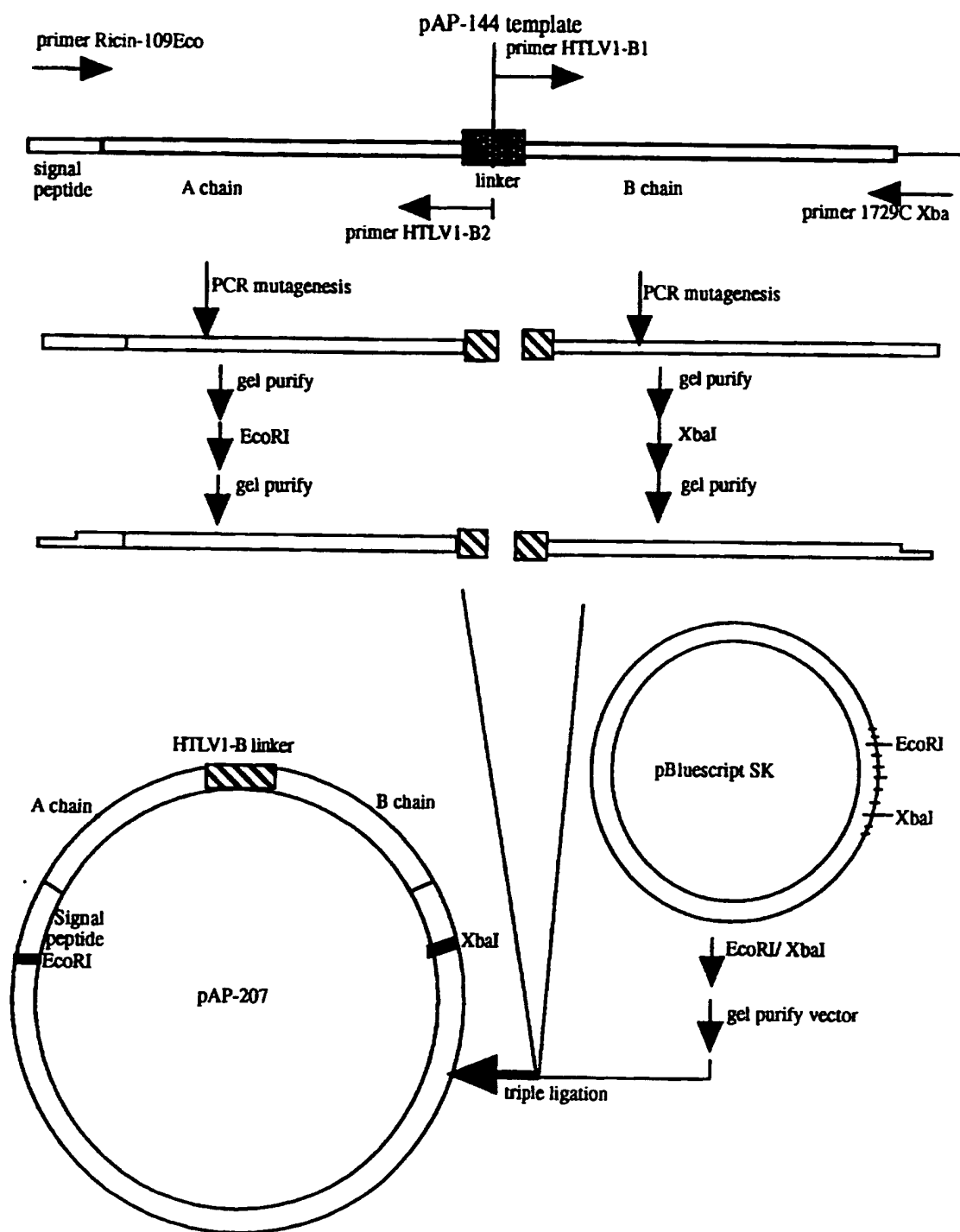
10 20 30 40 50  
1 GAATTCATGAAACCGGGAGGAAATACTATTGTAATATGGATGTATGCAGT  
CTTAAGTACTTTGGCCCTCCTTTATGATAACATTATACCTACATACGTCA  
51 GGCAACATGGCTTTGTTTGGATCCACCTCAGGGTGGTCTTTCACATTAG  
CCGTTGTACCGAAACAAAACCTAGGTGGAGTCCCACCAGAAAGTGAATC  
101 AGGATAACAACATATTCCCCAAACAATACCCAATTATAAACTTTACCACA  
TCCTATTGTTGTATAAGGGGTTGTTATGGGTTAATATTTGAAATGGTGT  
151 GCGGGTGCCACTGTGCAAAGCTACACAACTTTATCAGAGCTGTTTCGCGG  
CGCCACGGTGACACGTTTCGATGTGTTGAAATAGTCTCGACAAGCGCC  
201 TCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTCGCAA  
AGCAAATTGTTGACCTCGACTACACTCTGTACTATATGGTCACAACGGTT  
251 ACAGAGTTGGTTTGCCCTATAAACCACGGTTTATTTTAGTTGAACCTCA  
TGTCTCAACCAAACGGATATTGGTTGCCAAATAAAATCAACTTGAGAGT  
301 AATCATGCAGAGCTTTCTGTTACATTAGCGCTGGATGTACCAATGCATA  
TTAGTACGTCTCGAAAGACAATGTAATCGCGACCTACAGTGGTTACGTAT  
351 TGTGGTCGGCTACCGTGCTGGAATAGCGCATATTTCTTTTCATCTCTGACA  
ACACCAGCCGATGGCAGACCTTTATCGCGTATAAAGAAAGTAGGACTGT  
401 ATCAGGAAGATGCAGAAGCAATCACTCATCTTTTCACTGATGTTCAAAAT  
TAGTCCTTCTACGTCTTCGTTAGTGAGTAGAAAAGTGACTACAAGTTTTA  
451 CGATATACATTTCGCTTTGGTGGTAATTATGATAGACTTGAACAACCTGC  
GCTATATGTAAGCGGAAACCACCAATTAATACTATCTGAACCTGTTGAACG  
501 TGGTAATCTGAGAGAAAATATCGAGTTGGGAAATGGTCCACTAGAGGAGG  
ACCATTAGACTCTCTTTATAGCTCAACCCCTTACCAGGTGATCTCCTCC  
551 CTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAGCTTCCAAC  
GATAGAGTCGCGAAATAATAATGTCATGACCACCGTGAGTCGAAGGTTGA  
601 CTGGCTCGTTCCCTTTATAATTTGCATCCAAATGATTCAGAAGCAGCAAG  
GACCGAGCAAGGAAATATTAAACGTAGGTTTACTAAAGTCTTCGTCTGTTTC  
651 ATTCCAATATATTGAGGGAGAAATGCGCACGAGAATTAGGTACAACCGGA  
TAAGGTTATATAACTCCCTCTTTACGCGTGCTCTTAATCCATGTTGGCT  
701 GATCTGCACCAGATCCTAGCGTAATTACACTTGAGAATAGTTGGGGGAGA  
CTAGACGTGGTCTAGGATCGCATTAATGTGAACTCTTATCAACCCCTCT  
751 CTTTCCACTGCAATTCAAGAGTCTAACCAAGGAGCCTTTGCTAGTCCAAT  
GAAAGGTGACGTTAAGTTCTCAGATTGGTTCTCGGAAACGATCAGGTTA  
801 TCAACTGCAAAGACGTAATGGTTCCAAATTCAGTGTGTACGATGTGAGTA  
AGTTGACGTTTCTGCATTACCAAGGTTAAGTCACACATGCTACACTCAT  
851 TATTAATCCCTATCATAGCTCTCATGGTGATAGATGCGCACCTCCACCA  
ATAATTAGGGATAGTATCGAGAGTACCACATATCTACGCGTGGAGGTGGT  
901 TCGTCACAGTTTCTGCGCCTCAAGTGCTACCGGTGATGCATCCTAATGC  
AGCAGTGTCAAAGACGCGGAGTTCAGATGGCCACTACGTAGGATTACG  
951 TGATGTTTGTATGGATCCTGAGCCCATAGTGGTATCGTAGGTGGAATG

SUBSTITUTE SHEET (RULE 26)

31/47  
**FIGURE 16D (CONT'D)**

ACTACAAACATACCTAGGACTCGGGTATCACGCATAGCATCCAGCTTTAC  
1001 GTCTATGTGTTGATGTTAGGGATGGAAGATTCCACAACGGAAACGCAATA  
CAGATACACAACCTACAATCCCTACCTTCTAAGGTGTTGCCTTTGCGTTAT  
1051 CAGTTGTGGCCATGCAAGTCTAATACAGATGCAAATCAGCTCTGGACTTT  
GTCAACACCGGTACGTTAGATTATGTTACGTTTAGTCGAGACCTGAA  
1101 GAAAAGAGACAATACTATTGATCTAATGGAAAGTGTAACTACTTACG  
CTTTCTCTGTTATGATAAGCTAGATTACCTTTCACAAATTGATGAATGC  
1151 GGTACAGTCCGGGAGTCTATGTGATGATCTATGATTGCAATACTGCTGCA  
CCATGTCAGGCCCTCAGATACACTACTAGATACTAACGTTATGACGACGT  
1201 ACTGATGCCACCCGCTGGCAAATATGGGATAATGGAACCATCATAAATCC  
TGACTACGGTGGGCGACCGTTTATACCTATTACCTTGGTAGTATTTAGG  
1251 CAGATCTAGTCTAGTTTATAGCAGCGACATCAGGGAACAGTGGTACCACAC  
GTCTAGATCAGATCAAAATCGTCGCTGTAGTCCCTTGTCAACCATGGTGTG  
1301 TTACAGTGCAAACCAACATTTATGCCGTTAGTCAAGGTTGGCTTCCTACT  
AATGTCACGTTTGGTTGTAAATACGGCAATCAGTTCCAACCGAAGGATGA  
1351 AATAATACACAACCTTTTGTACAACCATTTGTTGGGCTATATGGTCTGTG  
TTATTATGTGTTGGAAAACAATGTTGGTAACAACCCGATATACCAGACAC  
1401 CTTGCAAGCAAATAGTGGACAAGTATGGATAGAGGACTGTAGCAGTGAAA  
GAACGTTGTTTATCACCTGTTTATACCTATCTCCTGACATCGTCACTTT  
1451 AGGCTGAACAACAGTGGGCTCTTTATGCAGATGGTTCAATACGTCCTCAG  
TCCGACTTGTGTCACCCGAGAAATACGCTACCAAGTTATGCAGGAGTC  
1501 CAAAACCGAGATAATTGCCCTTACAAGTGATTCTAATATACGGGAAACAGT  
GTTTTGGCTCTATTAAACGGAATGTTCACTAAGATTATATGCCCTTTGTCA  
1551 TGTTAAGATCCTCTCTTGTGGCCCTGCATCCTCTGGCCAACGATGGATGT  
ACAATTCTAGGAGAGAAACACCGGACGTAGGAGACCGGTTGCTACCTACA  
1601 TCAAGAATGATGGAACCATTTTAAATTGTATAGTGGATTGGTGTAGAT  
AGTTCTTACTACCTTGGTAAAATTTAAACATATCACCTAACCAACAATCTA  
1651 GTGAGGCGATCGGATCCGAGCCTTAAACAAATCATTCTTTACCCCTCTCCA  
CACTCCGCTAGCCTAGGCTCGGAATTGTTTAGTAAGAAATGGGAGAGGT  
1701 TGGTGACCCAAACCAAATATGGTTACCATTATTTTGATAGACAGATTACT  
ACCACTGGGTTTGGTTTATACCAATGGTAATAAAACTATCTGTCTAATGA  
1751 CTCTTGCAAGTGTGTGTTCTGTCATGAAAAATAGATGGCTTAAATAAAAA  
GAGAACGTCACACACACAGGACGGTACTTTTATCTACCGAATTTATTTTT  
1801 GGACATTGTAAATTTTGTAACTGAAAGGACAGCAAGTTATATCGAATTCC  
CCTGTAACATTTAAACATTGACTTTCCTGTCGTTCAATATAGCTTAAGG  
1851 TGCAG  
ACGTC

32/47

**FIGURE 17A**

33/47

**FIGURE 17B****WT preproreclin linker**

primer HTLV1-B1

5' - GTGGTGCAACCTAAGAAATGCTGATGTTTGT - 3'

TCTTTGCTTATAAGGCCAGTGGTGCCCAATTTTAAT  
 AGAAACGAATATTCCGGTCACCCACGGTTTAAATTA

3' - AGCAGTGTCAAAGATTCTGATTCACGAT - 5'

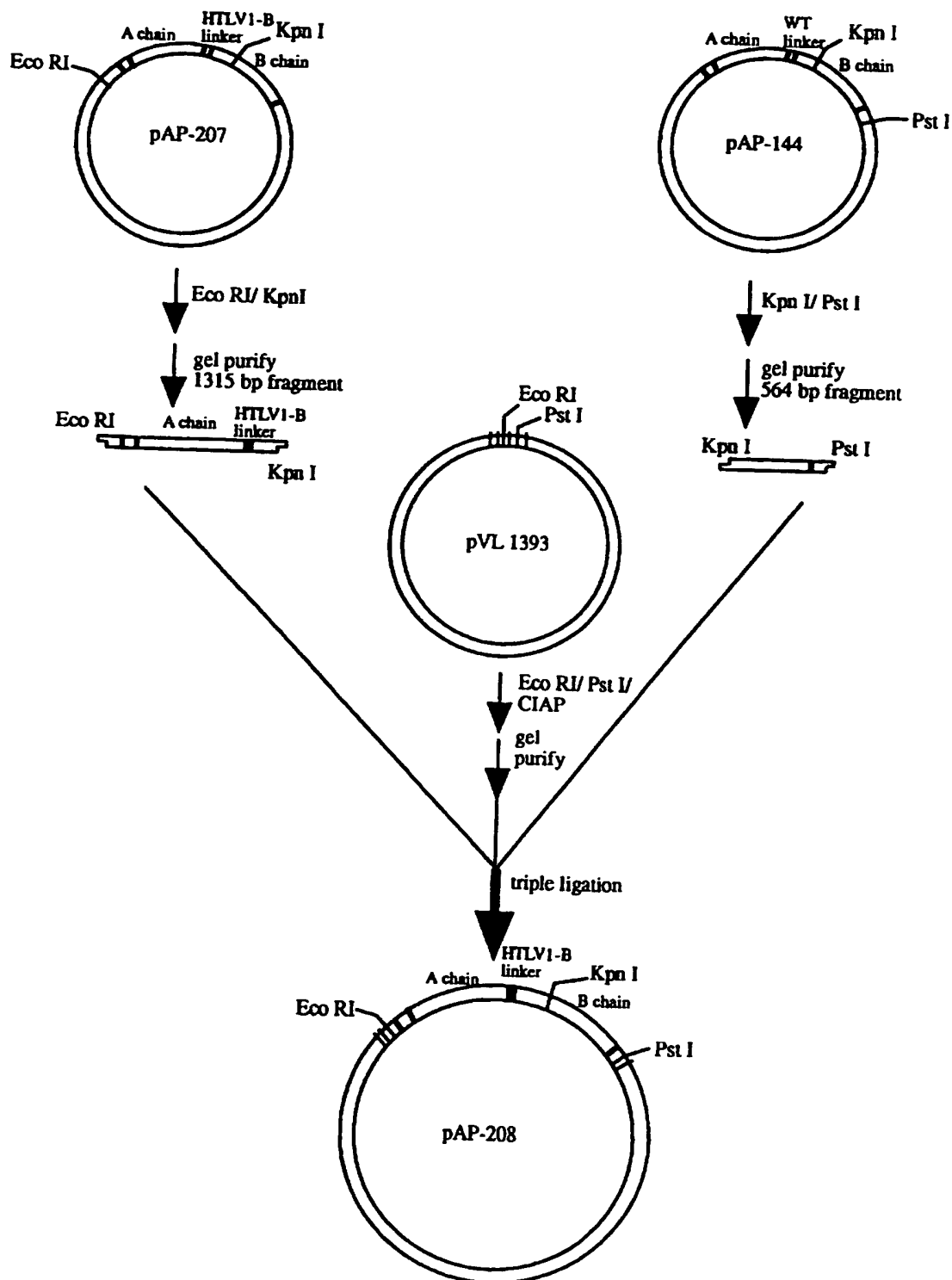
primer HTLV1-B2

PCR mutagenesis

ligate with pBluescript SK

PAP 207 linker  
 (HTLV1-B variant)

TCTAAGACTAAAGTGTAGTGGTGCAACCTAAGAAT  
 AGATTCTGATTTCACGATCACCACGGTTGGATTCTTA

34/47  
**FIGURE 17C**

SUBSTITUTE SHEET (RULE 26)

35/47

**FIGURE 17D**

10 20 30 40 50

1 GAATTCATGAAACCGGGAGGAAATACTATTGTAATATGGATGTATGCAGT  
CTTAAGTACTTTGGCCCTCCTTTATGATAACATTATACCTACATACGTCA

51 GGCAACATGGCTTTGTTTGGATCCACCTCAGGGTGGTCTTTCACATTAG  
CCGTTGTACCGAAACAAAACCTAGGTGGAGTCCCACCAGAAAGTGAATC

101 AGGATAACAACATATTCCTCCAAACAATACCCAATTATAAACTTTACCACA  
TCCTATTGTGTATAAGGGGTTTGTATGGGTTAATATTTGAAATGGTGT

151 GCGGGTGCCACTGTGCAAAGCTACACAAACTTTATCAGAGCTGTTTCGCGG  
CGCCACGGTGACACGTTTCGATGTGTTTGAAATAGTCTCGACAAGCGCC

201 TCGTTTAACTGGAGCTGATGTGAGACATGATATACCAGTGTTCGCAA  
AGCAAATGTTGACCTCGACTTACTCTGTACTATATGGTCACAACGGTT

251 ACAGAGTTGGTTTGCTTATAAACCAACGGTTTATTTTAGTTGAACTCTCA  
TGTCTCAACCAACGATATTTGGTTGCCAAATAAAATCAACTTGAGAGT

301 AATCATGCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATA  
TTAGTACGTCTCGAAAGACAATGTAATCGCGACCTACAGTGGTTACGTAT

351 TGTGGTGGCTACCGTGCTGGAAATAGCGCATATTTCTTTTCATCCTGACA  
ACACCAGCCGATGGCACGACCTTTATCGCGTATAAAGAAAGTAGGACTGT

401 ATCAGGAAGATGCAGAAGCAATCACTCATCTTTTCACTGATGTTCAAAT  
TAGTCCTTCTACGTCTTCGTTAGTGAGTAGAAAAGTGACTACAAGTTTTA

451 CGATATACATTTCGCTTTGGTGGTAAATTATGATAGACTTGAACAACCTGC  
GCTATATGTAAGCGGAAACCACCATTAATACTATCTGAACTTGTGTAACG

501 TGGTAATCTGAGAGAAAATATCGAGTTGGGAAATGGTCCACTAGAGGAGG  
ACCATTAGACTCTCTTTTATAGCTCAACCTTTACCAGGTGATCTCTCTCC

551 CTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAGCTTCCAAC  
GATAGAGTCCGGAATAATAATGTCATGACCACCGTGAGTCGAAGGTTGA

601 CTGGCTCGTTCCCTTTATAATTTGCATCCAAATGATTTCAGAAGCAGCAAG  
GACCGAGCAAGGAAATATTAAACGTAGGTTTACTAAAGTCTTCGTCTGTT

651 ATTCCAATATATTGAGGGAGAAATGCGCACGAGAATTAGGTACAACCGGA  
TAAGGTTATATAACTCCCTCTTTACGCGTGCTCTTAATCCATGTTGGCCT

701 GATCTGCACCAGATCCTAGCGTAATTACACTTGAGAATAGTTGGGGGAGA  
CTAGACGTGGTCTAGGATCGCATTAAATGTGAATCTTATCAACCCCTCT

751 CTTTCCACTGCAATTCAAGAGTCTAACCAAGGAGCCTTTGCTAGTCCAAT  
GAAAGGTGACGTTAAGTTCTCAGATTGGTTCCCTCGGAAACGATCAGGTTA

801 TCAACTGCAAAGACGTAATGGTTCCAAATTCAGTGTGTACGATGTGAGTA  
AGTTGACGTTCTGCATTACCAAGGTTTAAAGTCACACATGCTACACTCAT

851 TATTAATCCCTATCATAGCTCTCATGGTGTATAGATGCGCACCTCCACCA  
ATAATTAGGATAGTATCGAGAGTACCACATATCTACCGTGAGGTTGGT

901 TCGTCACAGTTTCTAAGACTAAAGTGCTAGTGGTGCAACCTAAGAATGC  
AGCAGTGTCAAAAGATTCTGATTTCACGATCACCAGTTGGATTCTTACG

951 TGATGTTTGTATGGATCCTGAGCCCATAGTGGTATCGTAGGTGCAAAATG  
ACTACAAACATACCTAGGACTCGGGTATCACGCATAGCATCCAGCTTTAC

SUBSTITUTE SHEET (RULE 26)



36/47  
**FIGURE 17D (CONT'D)**

1001 GTCTATGTGTTGATGTTAGGGATGGAAGATTCCACAACGGAAACGCAATA  
CAGATACACAACCTACAATCCCTACCTTCTAAGGTGTTGCCTTTGCGTTAT

1051 CAGTTGTGGCCATGCAAGTCTAATACAGATGCAAAATCAGCTCTGGACTTT  
GTCAACACCGGTACGTTTACAGATTATGTCACGTTTAGTCGAGACCTGAAA

1101 GAAAAGAGACAATACTATTTCGATCTAATGGAAGTGTCTTAACCTACTTACG  
CTTTTCTCTGTTATGATAAGCTAGATTACCTTTCACAAATTGATGAATGC

1151 GGTACAGTCCGGGAGTCTATGTGATGATCTATGATTGCAATACTGTGCA  
CCATGTCAGGCCCTCAGATACACTACTAGATACTAACGTTATGACGACGT

1201 ACTGATGCCACCCGCTGGCAAATATGGGATAATGGAACCATCATAAATCC  
TGACTACGGTGGGCGACCGTTTATACCTTATTACCTTGGTAGTATTAGG

1251 CAGATCTAGTCTAGTTTTAGCAGCGACATCAGGGAACAGTGGTACCACAC  
GTCTAGATCAGATCAAAATCGTCGCTGTAGTCCCTTGTCAACCATGGTGTG

1301 TTACAGTGCAAACCAACATTTATGCCGTTAGTCAAGGTTGGCTTCTACT  
AATGTCACGTTTGGTTGTAATACGGCAATCAGTTCCAACCGAAGGATGA

1351 AATAATACACAACCTTTTGTGTTACAACCATGTTGGGCTATATGGTCTGTG  
TTATTATGTGTTGGAAAACAATGTTGGTAACAACCGATATACCAGACAC

1401 CTTGCAAGCAAATAGTGGACAAGTATGGATAGAGGACTGTAGCAGTGAAA  
GAACGTTTCGTTTATCACCTGTTTCATACCTATCTCTGACATCGTCACTTT

1451 AGGCTGAACAACAGTGGGCTCTTTATGCAGATGGTTCAATACGTCCTCAG  
TCCGACTTGTGTCACCCGAGAAATACGTCCTACCAAGTTATGCAGGAGTC

1501 CAAAACCGAGATAATTGCCTTACAAGTGATTCTAATATACGGGAAACAGT  
GTTTTGGCTCTATTAACGGAATGTTCACTAAGATTATATGCCCTTTGTCA

1551 TGTTAAGATCCTCTCTTGTGGCCCTGCATCCTCTGGCCAACGATGGATGT  
ACAATTCTAGGAGAGAACACCGGACGTAGGAGACCGGTTGCTACCTACA

1601 TCAAGAATGATGGAACCATTTTAAATTTGTATAGTGGATTGGTGTAGAT  
AGTTCTTACTACCTTGGTAAATTTAAACATATCACCTAACCAATCTA

1651 GTGAGGCGATCGGATCCGAGCCTTAAACAAATCATTCTTTACCCCTCTCCA  
CACTCCGCTAGCCTAGGCTCGGAATTTGTTTAGTAAGAAATGGGAGAGGT

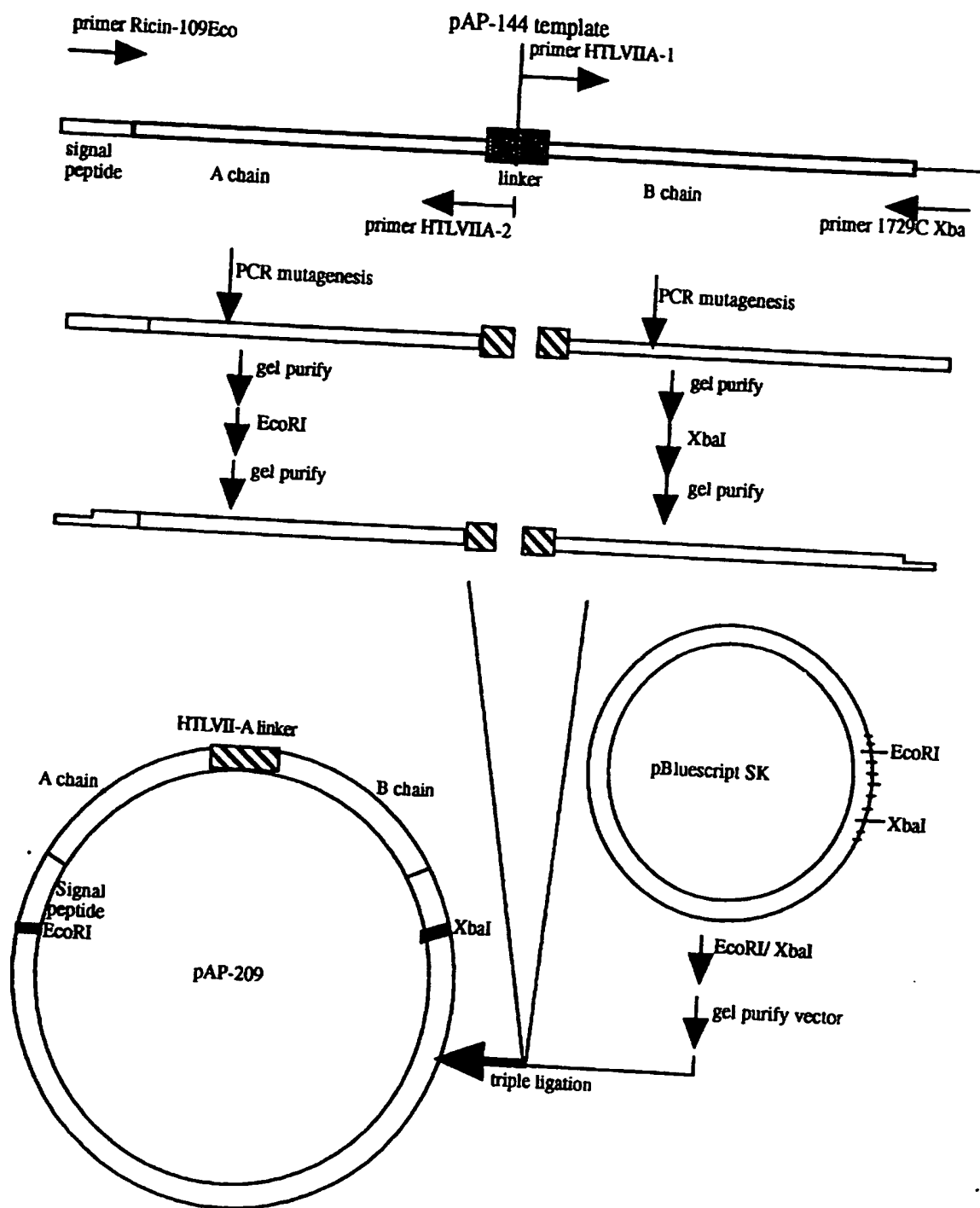
1701 TGGTGACCCAAACCAATATGGTTACCATTATTTTGATAGACAGATTACT  
ACCACTGGGTTTGGTTTATACCAATGGTAATAAACTATCTGTCTAATGA

1751 CTCTGCAAGTGTGTGTCTGCGCATGAAAATAGATGGCTTAAATAAAAA  
GAGAACGTCACACACAGGACGGTACTTTTATCTACCGAATTTATTTTT

1801 GGACATTGTAAATTTTGTAACTGAAAGGACAGCAAGTTATATCGAATTCC  
CCTGTAACATTTAAACATGACTTTCCTGTCTGTTCAATATAGCTTAAGG

1851 TGCAG  
ACGTC

37/47

**FIGURE 18A**

SUBSTITUTE SHEET (RULE 26)

38/47

**FIGURE 18B****WT preproreclin linker**

primer HTLV11-A1

5'- GTGGTGCAACCTAGGAATGCTGATGTTGT -3'

TCTTTGCTTATAAGGCCA  
 AGAAACGAATATTCGGT

3'- AGCAGTGTCAAAAGATTCTGATTCACGAT-5'

primer HTLV11-A2

PCR mutagenesis

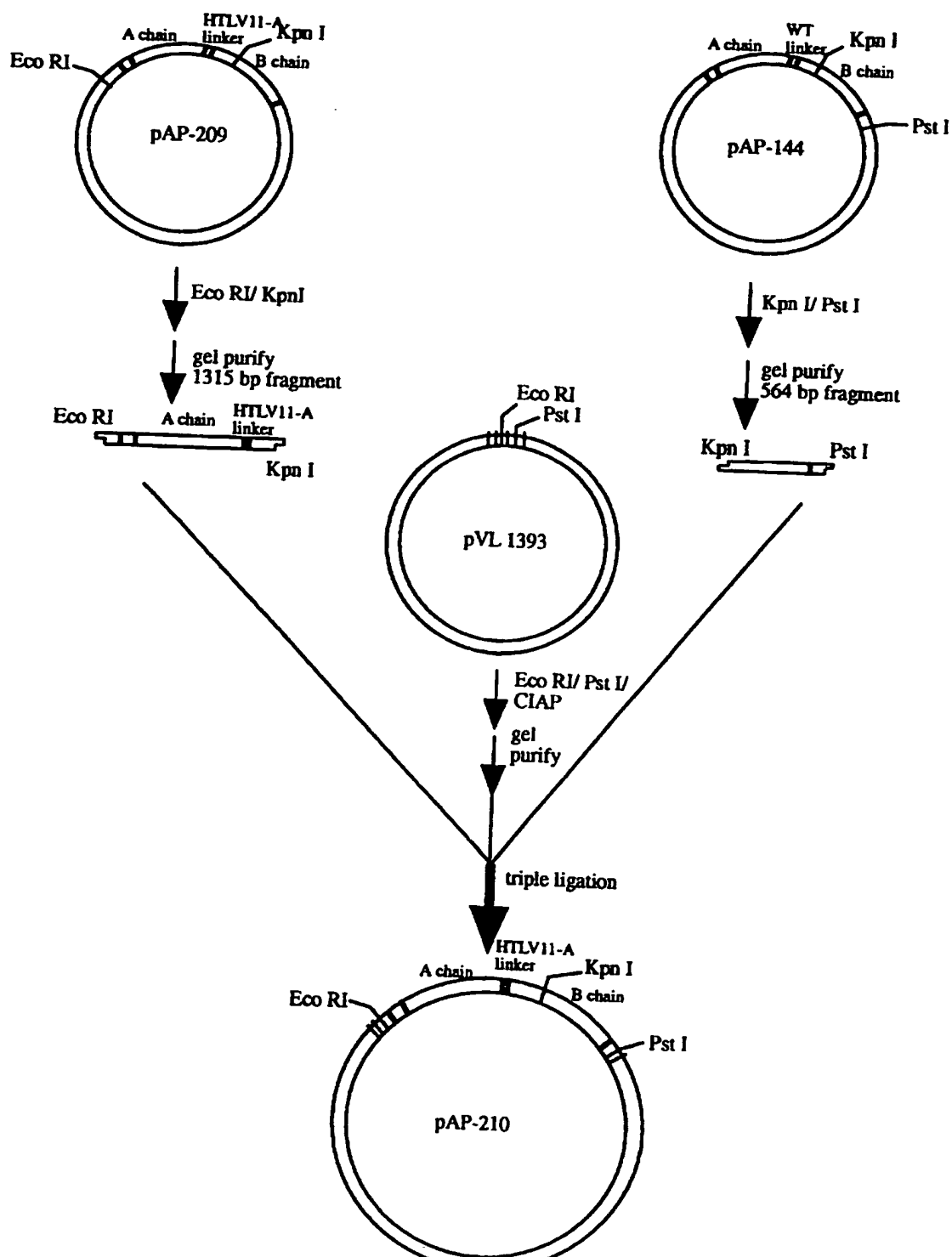
ligate with pBluescript SK

pAP 209 linker

(HTLV11-A variant)

TCTAAGACTAAAGTGCTAGTGCGCAACCTAGGAAT  
 AGATTCTGATTCACGATCACCGTTGGATCCTTA

39/47

**FIGURE 18C**

SUBSTITUTE SHEET (RULE 26)

40/47

**FIGURE 18D**

10 20 30 40 50

1 GAATTCATGAAACCGGGAGGAAATACTATTGTAATATGGATGTATGCAGT  
CTTAAGTACTTTGGCCCTCCTTTATGATAACATTATACCTACATACGTCA

51 GGCAACATGGCTTTGTTTGGATCCACCTCAGGGTGGTCTTTCACATTAG  
CCGTGTACCGAAACAAAACCTAGGTGGAGTCCCACCAGAAAGTGAATC

101 AGGATAACAACATATTCCCCAAACAATACCCAATTATAAACTTTACCACA  
TCCTATTGTTGTATAAGGGGTTTGTATGGGTAAATATTTGAAATGGTGT

151 GCGGGTGCCACTGTGCAAAGCTACACAACTTTATCAGAGCTGTTGCGGG  
CGCCACGGTGACACGTTTCGATGTGTTGAAATAGTCTCGACAAGCGCC

201 TCGTTTAACAACCTGGAGCTGATGTGAGACATGATATACCAGTGTGCCAA  
AGCAAATTGTTGACCTCGACTACACTCTGTACTATATGGTCACAACGGTT

251 ACAGAGTTGGTTTGCCCTATAAACCAACGGTTTATTTAGTTGAACTCTCA  
TGTCTCAACCAACGATATTGTTGCCAAATAAAATCAACTTGAGAGT

301 AATCATGCAGAGCTTCTGTTACATTAGCGCTGGATGTCACCAATGCATA  
TTAGTACGTCTCGAAAGACAATGTAATCGCGACCTACAGTGGTTACGTAT

351 TGTGGTTCGGCTACCGTGCTGGAAATAGCGCATATTTCTTTCATCCTGACA  
ACACCAGCCGATGGCAGCAGCTTTATCGCGTATAAAGAAAGTAGGACTGT

401 ATCAGGAAGATGCAGAAGCAATCACTCATCTTTCCTACTGATGTTCAAAAT  
TAGTCCTTCTACGTCTTCGTTAGTGAGTAGAAAAGTGACTACAAGTTTAA

451 CGATATACATTCGCCTTTGGTGGTAATTATGATAGACTTGAACAACTTGC  
GCTATATGTAAGCGGAAACCACCATTAATACTATCTGAACTTGTGAAACG

501 TGGTAATCTGAGAGAAAATATCGAGTTGGGAAATGGTCCACTAGAGGAGG  
ACCATTAGACTCTCTTTTATAGCTCAACCCTTTACCAGGTGATCTCCTCC

551 CTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAGCTTCCAAC  
GATAGAGTCGCGAAATAATAATGTCATGACCACCGTGAGTCGAAGGTTGA

601 CTGGCTCGTTCTTTTATAATTTGCATCCAAATGATTTGAGAAGCAGCAAG  
GACCGAGCAAGGAAATATTAAACGTAGGTTTACTAAAGTCTTCGTCGTTT

651 ATTCCAATATATTGAGGGAGAAATGCGCACGAGAATTAGGTACAACCGGA  
TAAGGTTATATACTCCCTCTTTACGCGTGCTCTTAATCCATGTTGGCCT

701 GATCTGCACCAGATCCTAGCGTAATTACACTTGAGAATAGTTGGGGGAGA  
CTAGACGTGGTCTAGGATCGCATTAAATGTGAACTCTTATCAACCCCTCT

751 CTTTCCACTGCAATTCAAGAGTCTAACCAAGGAGCCTTTGCTAGTCCAAT  
GAAAGGTGACGTTAAGTTCTCAGATTGGTTCTCGGAAACGATCAGGTTA

801 TCAACTGCAAAGACGTAATGGTTCCAAATTCAGTGTGTACGATGTGAGTA  
AGTTGACGTTTCTGCATTACCAAGGTTAAGTCACACATGCTACACTCAT

851 TATTAATCCCTATCATAGCTCTCATGGTGTATAGATGCGCACCTCCACCA  
ATAATTAGGGATAGTATCGAGAGTACCACATATCTACGCGTGGAGGTGGT

901 TCGTCACAGTTTCTAAGACTAAAGTGCTAGTGGTGCAACCTAGGAATGC  
ACGAGTGTCAAAAGATTCTGATTTACGATCACCAGTTGGATCCTTACG

951 TGATGTTTGTATGGATCCTGAGCCCATAGTGCATCGTAGGTGCAAAATG  
ACTACAAACATACCTAGGACTCGGGTATCACGCATAGCATCCAGCTTTAC

SUBSTITUTE SHEET (RULE 26)

41/47

FIGURE 18D (CONT'D)

1001 GTCTATGTGTTGATGTTAGGGATGGAAGATTCCACAACGGAAACGCAATA  
CAGATACACAACACTACAATCCCTACCTTCTAAGGTGTTGCCTTTGCGTTAT

1051 CAGTTGTGGCCATGCAAGTCTAATACAGATGCAAATCAGCTCTGGACTTT  
GTCAACACCGGTACGTTTCAGATTATGTCTACGTTTAGTCGAGACCTGAAA

1101 GAAAAGAGACAATACTATTTCGATCTAATGGAAGTGTTTAACTACTTACG  
CTTTTCTCTGTTATGATAAGCTAGATTACCTTTCACAAATTGATGAATGC

1151 GGTACAGTCCGGGAGTCTATGTGATGATCTATGATTGCAATACTGCTGCA  
CCATGTCAGGCCCTCAGATACACTACTAGATACTAACGTTATGACGACGT

1201 ACTGATGCCACCCGCTGGCAAATATGGGATAATGGAACCATCATAAATCC  
TGACTACGGTGGGCGACCGTTTATACCTATTACCTTGGTAGTATTTAGG

1251 CAGATCTAGTCTAGTTTTAGCAGCGACATCAGGGAACAGTGGTACCACAC  
GTCTAGATCAGATCAAAATCGTCGCTGTAGTCCCTTGTCACCATGGTGTG

1301 TTACAGTGCAAACCAACATTTATGCCGTTAGTCAAGGTTGGCTTCCTACT  
AATGTCACGTTTGGTTGTAAATACGGCAATCAGTTCCAACCGAAGGATGA

1351 AATAATACACAACCTTTTGTTCACAACCATTTGTTGGGCTATATGGTCTGTG  
TTATTATGTGTTGGAAAACAATGTTGGTAACAACCCGATATACCAGACAC

1401 CTTGCAAGCAAATAGTGGACAAGTATGGATAGAGGACTGTAGCAGTGAAA  
GAACGTTTCGTTTATCACCTGTTTCATACCTATCTCCTGACATCGTCACCTTT

1451 AGGCTGAACAACAGTGGGCTCTTTATGCAGATGGTTCAATACGTCCTCAG  
TCCGACTTGTGTCACCCGAGAAATACGTCTACCAAGTTATGCAGGAGTC

1501 CAAAACCGAGATAATTGCCTTACAAGTGATTCTAATATACGGGAAACAGT  
GTTTTGGCTCTATTAACGGAATGTTCACTAAGATTATATGCCCTTTGTCA

1551 TGTTAAGATCCTCTCTTGTGGCCCTGCATCCTCTGGCCAACGATGGATGT  
ACAAATTCTAGGAGAGAACACCGGGACGTAGGAGACCGGTTGCTACCTACA

1601 TCAAGAATGATGGAACCATTTTAAATTTGTATAGTGGATTGGTGTAGAT  
AGTTCTTACTACCTTGGTAAAATTTAAACATATCACCTAACCAATCTA

1651 GTGAGGCGATCGGATCCGAGCCTTAAACAAATCATTCTTTACCTCTCCA  
CACTCCGCTAGCCTAGGCTCGGAATTTGTTTAGTAAGAAATGGGAGAGGT

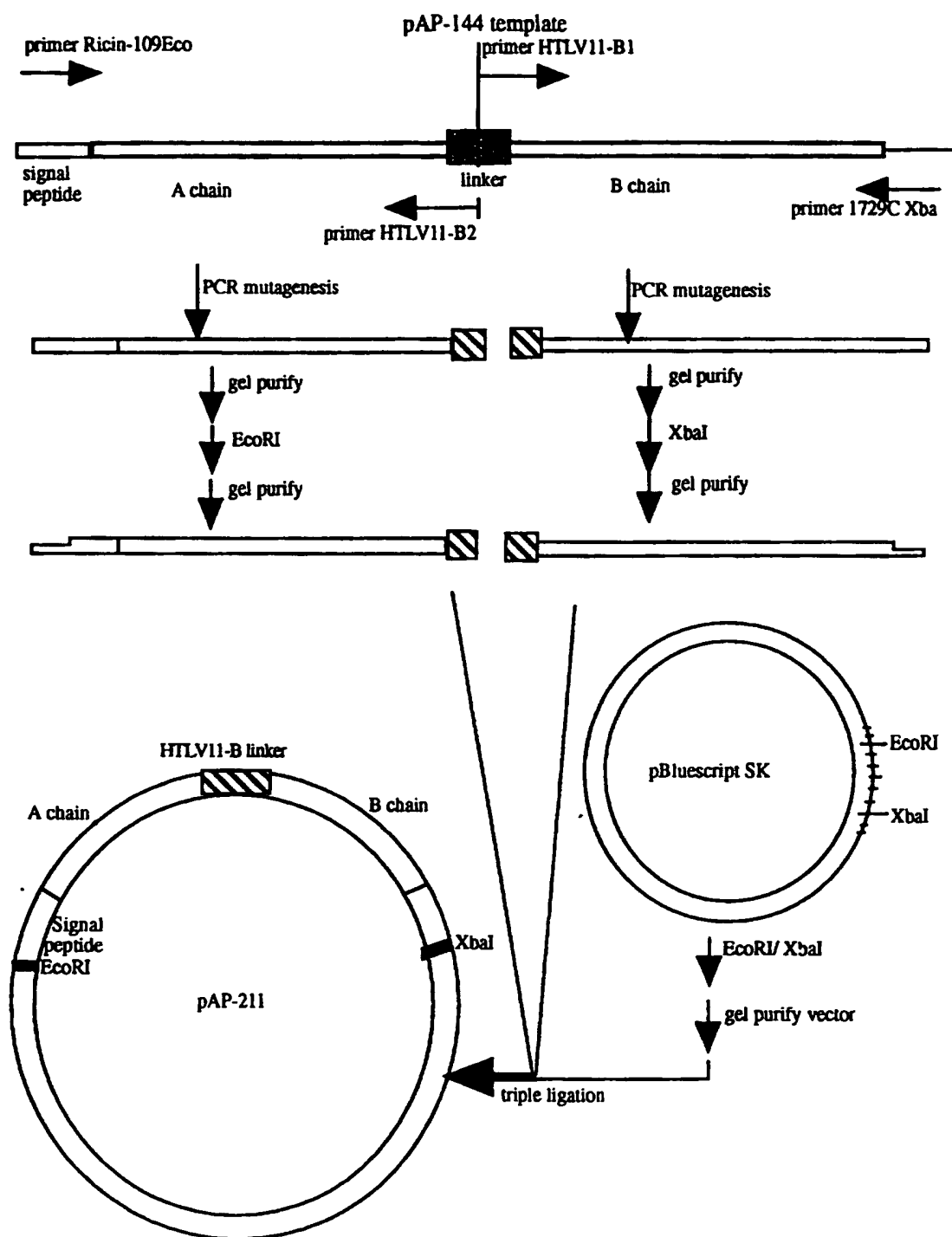
1701 TGGTGACCCAAACCAAATATGGTTACCATTATTTTGATAGACAGATTACT  
ACCCTGGGTTTGGTTTATACCAATGGTAATAAACTATCTGTCTAATGA

1751 CTCTTGCAGTGTGTGTCTCTGCCATGAAAATAGATGGCTTAAATAAAAA  
GAGAACGTCACACACACAGGACGGTACTTTTATCTACCGAATTTATTTTT

1801 GGACATTGTAAATTTTGTAACTGAAAGGACAGCAAGTTATATCGAATTCC  
CCTGTAACATTTAAACATTGACTTTCCTGTCGTTCAATATAGCTTAAGG

1851 TGCAG  
ACGTC

42/47

**FIGURE 19A**

SUBSTITUTE SHEET (RULE 26)

43/47

**FIGURE 19B****WT preproreclin linker**

primer HTLV11-B1

5' - CCGATACTACATCCTAATGCTGATGTTTGT -3'

TCTTTGCTTATAAGGCCAGTGTGCCAAATTTTAAT  
 AGAAACGAATATTCGGTCACCCACGGTTTAAATTA

3' - ACGAGTGTCAAAAGATGCTGAGTTACAAAG-5'

primer HTLV11-B2

PCR mutagenesis

ligate with pBluescript SK

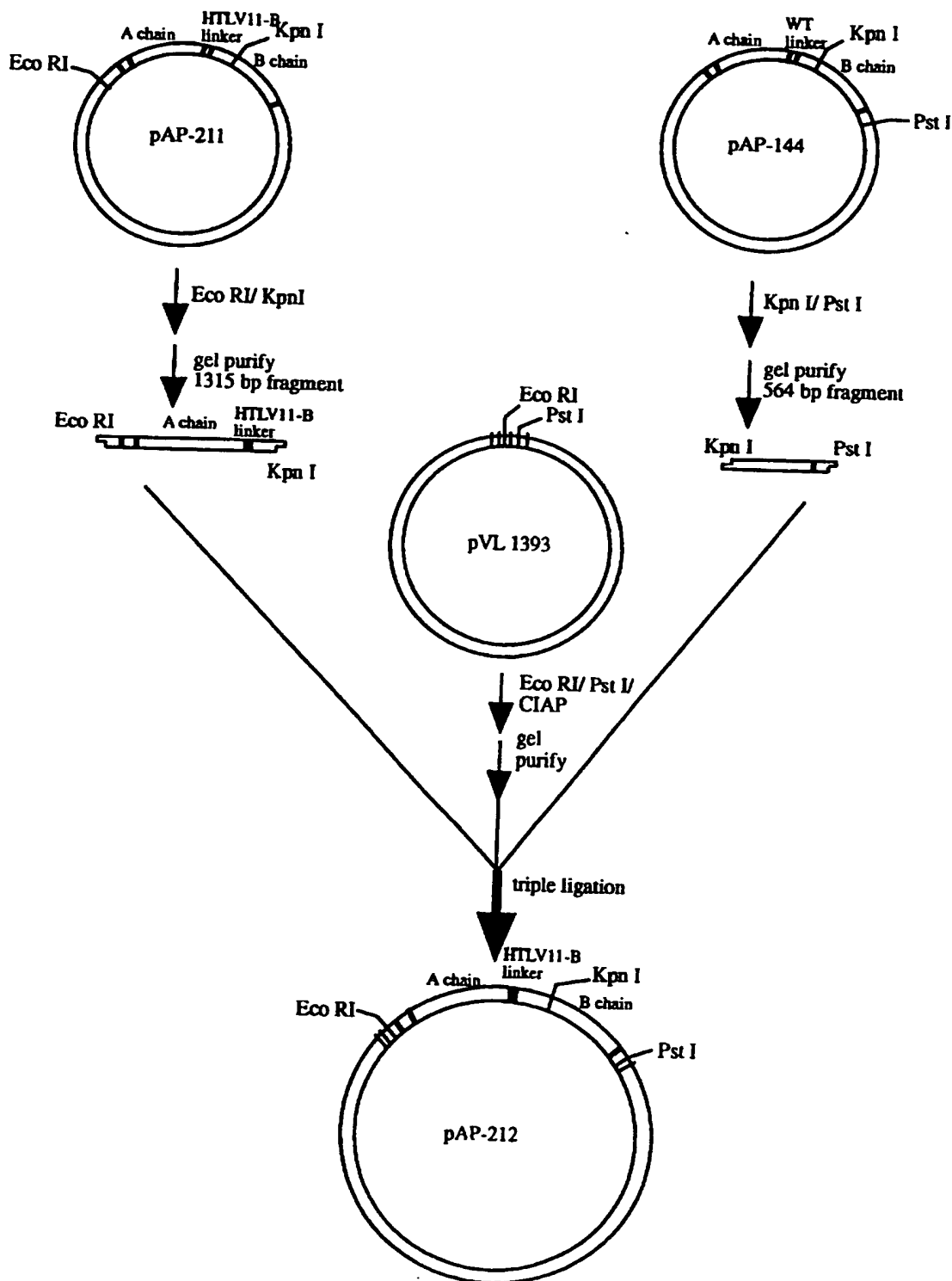
pAP 211 linker

(HTLV11-B variant)

TCTACGACTCAATGTTCCCGATACTACATCCTAAT  
 AGATGCTGAGTTACAAAGGCTATGATGTAGGATTA



44/47

**FIGURE 19C**

SUBSTITUTE SHEET (RULE 26)

45/47

FIGURE 19D

10 20 30 40 50

1 GAATTCATGAAACCGGAGGAAATACTATTGTAATATGGATGTATGCAGT  
CTTAAGTACTTTGGCCCTCCTTTATGATAACATTATACCTACATACGTCA

51 GGCAACATGGCTTTGTTTTGGATCCACCTCAGGGTGGTCTTTCACATTAG  
CCGTTGTACCGAAACAAAACCTAGGTGGAGTCCCACCAGAAAGTGTAAATC

101 AGGATAACAACATATTCCCCAAACAATACCCAATTATAAACTTTACCACA  
TCCTATTGTTGTATAAGGGGTTGTTATGGGTTAATATTTGAAATGGTGT

151 GCGGGTGCCACTGTGCAAAGCTACACAACTTTATCAGAGCTGTTTCGCGG  
CGCCACGGTGACACGTTTCGATGTGTTGAAATAGTCTCGACAAGCGCC

201 TCGTTTAAACAACCTGGAGCTGATGTGAGACATGATATACCAGTGTTCGCAA  
AGCAAATGTTGACCTCGACTACACTCTGTACTATATGGTCACAACGGTT

251 ACAGAGTTGGTTTGCCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCA  
TGCTCAACCAACGGATATTTGGTTGCCAAATAAAATCAACTTGAGAGT

301 AATCATGCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATA  
TTAGTACGTCTCGAAAGACAATGTAATCGCGACCTACAGTGGTTACGTAT

351 TGTGGTCGGCTACCGTGCTGGAAATAGCGCATATTTCTTTTCATCCTGACA  
ACACCAGCCGATGGCACGACCTTTATCGCGTATAAAGAAAGTAGGACTGT

401 ATCAGGAAGATGCAGAAGCAATCACTCATCTTTTCACTGATGTTCAAAAT  
TAGTCCTTCTACGTCTTCGTTAGTGAGTAGAAAAGTACTACAAGTTTTA

451 CGATATACATTTCGCCTTTGGTGGTAATTATGATAGACTTGAACAACTTGC  
GCTATATGTAAGCGGAAACCACCATTAATACTATCTGAACCTGTTGAACG

501 TGGTAATCTGAGAGAAAATATCGAGTTGGGAAATGGTCCACTAGAGGAGG  
ACCATTAGACTCTCTTTTATAGCTCAACCTTTACCAGGTGATCTCCTCC

551 CTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAGCTTCCAAC  
GATAGAGTCGCGAAATAATAATGTCATGACCACCGTGAGTCGAAGGTTGA

601 CTGGCTCGTTCTCTTTATAATTTGCATCCAAATGATTTTCAAGCAGCAAG  
GACCGAGCAAGGAAATATTAAACGTAGGTTTACTAAAGTCTTCGTCTGTT

651 ATTCCAATATATTGAGGGAGAAATGCGCACGAGAAATTAGGTACAACCGGA  
TAAGGTTATATAACTCCCTCTTTACGCGTGCTCTTAATCCATGTTGGCCT

701 GATCTGCACCAGATCCTAGCGTAATTACACTTGAGAATAGTTGGGGGAGA  
CTAGACGTGGTCTAGGATCGCATTAAATGTGAACCTTTATCAACCCCTCT

751 CTTTCCACTGCAATTCAAGAGTCTAACCAAGGAGCCTTTGCTAGTCCAAT  
GAAAGGTGACGTTAAGTTCTCAGATTGGTTCTCGGAAACGATCAGGTTA

801 TCAACTGCAAAGACGTAATGGTTCCAAATTCAGTGTGTACGATGTGAGTA  
AGTTGACGTTTCTGCATTACCAAGGTTAAGTCACACATGCTACACTCAT

851 TATTAATCCCTATCATAGCTCTCATGGTGTATAGATGCGCACCTCCACCA  
ATAATTAGGGATAGTATCGAGAGTACCACATATCTACGCGTGGAGGTGGT

901 TCGTCACAGTTTCTACGACTCAATGTTTCCCGATACTACATCCTAATGC  
AGCAGTGTCAAAGATGCTGAGTTACAAAGGCTATGATGTAGGATTACG

951 TGATGTTGTATGGATCCTGAGCCCATAGTGCGTATCGTAGGTGGAATG  
ACTACAAACATACCTAGGACTCGGGTATCACGCATAGCATCCAGCTTTAC

SUBSTITUTE SHEET (RULE 26)

46/47  
**FIGURE 19D (CONT'D)**

1001 GTCTATGTGTTGATGTTAGGGATGGAAGATTCCACAACGGAAACGCAATA  
CAGATACACAAC TACAATCCCTACCTTCTAAGGTGTTGCCTTTGCGTTAT

1051 CAGTTGTGGCCATGCAAGTCTAATACAGATGCAAATCAGCTCTGGACTTT  
GTCAACACCGGTACGTTTACAGATTATGTCTACGTTTAGTCGAGACCTGAAA

1101 GAAAAGAGACAATACTATTCGATCTAATGGAAAGTGTTTAACTACTTACG  
CTTTTCTCTGTTATGATAAGCTAGATTACCTTTTACAAAATTGATGAATGC

1151 GGTACAGTCCGGGAGTCTATGTGATGATCTATGATTGCAATACTGCTGCA  
CCATGTGAGGCCCTCAGATACACTACTAGATACTAACGTTATGACGACGT

1201 ACTGATGCCACCCGCTGGCAAATATGGGATAATGGAACCATCATAAATCC  
TGACTACGGTGGGCGACCGTTTATACCTATTACCTTGGTAGTATTTAGG

1251 CAGATCTAGTCTAGTTT TAGCAGCGACATCAGGGAACAGTGGTACCACAC  
GTCTAGATCAGATCAAAATCGTCGCTGTAGTCCCTTGTACCATGGTGTG

1301 TTACAGTGCAAACCAACATTTATGCCGTTAGTCAAGGTTGGCTTCCTACT  
AATGTCACGTTTGGTGTAAATACGGCAATCAGTTCCAACCGAAGGATGA

1351 AATAATACACAACCTTTTGTGTTACAACCATGTTGGGCTATATGGTCTGTG  
TTATATGTGTTGGAAAACAATGTTGGTAACAACCCGATATACCAGACAC

1401 CTTGCAAGCAAATAGTGGACAAGTATGGATAGAGGACTGTAGCAGTGAAA  
GAACGTTTCGTTTATCACCTGTTTATACCTATCTCCTGACATCGTCACTTT

1451 AGGCTGAACAACAGTGGGCTCTTTATGCAGATGGTTCAATACGTCCTCAG  
TCCGACTTGTGTGTCACCCGAGAAATACGTCCTACCAAGTTATGCAGGAGTC

1501 CAAAACCGAGATAATTGCCTTACAAGTGATTCTAATATACGGGAAACAGT  
GTTTGGCTCTATTAACGGAATGTTCACTAAGATTATATGCCCTTTGTCA

1551 TGTTAAGATCCTCTCTTGTGGCCCTGCATCCTCTGGCCAACGATGGATGT  
ACAATTCTAGGAGAGAACACCGGGACGTAGGAGACCGGTTGCTACCTACA

1601 TCAAGAATGATGGAACCATTTTAAATTTGTATAGTGGATTGGTGTAGAT  
AGTTCTTACTACCTTGGTAAAATTTAAACATATCACCTAACCACAATCTA

1651 GTGAGGCGATCGGATCCGAGCCTTAAACAAATCATCTTTTACCCTCTCCA  
CACTCCGCTAGCCTAGGCTCGGAATTTGTTTAGTAAGAAATGGGAGAGGT

1701 TGGTGACCCAAACCAATATGGTTACCATTATTTTGATAGACAGATTACT  
ACCACTGGGTTTGGTTTATACCAATGGTAATAAACTATCTGTCTAATGA

1751 CTCTTGCAGTGTGTGTGTCCTGCCATGAAAATAGATGGCTTAAATAAAAA  
GAGAACGTACACACACAGGACGGTACTTTTATCTACCGAATTTATTTT

1801 GGACATTGTAAATTTTGTAACTGAAAGGACAGCAAGTTATATCGAATTCC  
CCTGTAACATTTAAACATTGACTTTCCTGTCGTTCAATATAGCTTAAGG

1851 TGCAG  
ACGTC

47/47

**FIGURE 20**

Wild type Ricin linker: A chain- S L L I R P V V P N F N -B chain

pAP-205 linker: A chain- S A P Q V L P V M H P N -B chain  
pAP-206  
(HTLV1-A linker)

pAP-207 linker: A chain- S K T K V L V V Q P K N -B chain  
pAP-208  
(HTLV1-B linker)

pAP-209 linker: A chain- S I R K I L F L D G I N -B chain  
pAP-210  
(HTLV11-A linker)

pAP-211 linker: A chain- S T T Q C F P I L H P N -B chain  
pAP-212  
(HTLV11-B linker)

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 97/00288

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/29 C12N15/62 C12N15/70 C12N15/86 A61K38/16

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WESTBY M ET AL: "PREPARATION AND CHARACTERIZATION OF RECOMBINANT PRORICIN CONTAINING AN ALTERNATIVE PROTEASE-SENSITIVE LINKER SEQUENCE" BIOCONJUGATE CHEMISTRY, vol. 3, no. 5, 1 January 1992, pages 375-381, XP000578216 cited in the application see the whole document	1-28
Y	LEPPLA S. ET AL.: "Development of anthrax-toxin based fusion proteins for targeting of HIV-1-infected cells" ZENTRALBLATT FÜR BAKTERIOLOGIE, vol. 24, 1994, pages 431-442, XP002041056 see the whole document	1-28

-/-

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

\* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"A" document member of the same patent family

Date of the actual completion of the international search

1 October 1997

Date of mailing of the international search report

15.10.97

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,  
Fax: (+31-70) 340-3016

Authorized officer

Kania, T

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 97/00288

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>PETTIT S. ET AL.: "Analysis of retroviral protease cleavage sites reveals two types of cleavage sites and the structural requirements of the P1 amino acid" THE JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 266, no. 22, 5 August 1991, pages 14539-14547, XP002041058 cited in the application see the whole document</p> <p>---</p>	5,8,18, 20
A	<p>EP 0 466 222 A (DOWELANCO) 15 January 1992 cited in the application see the whole document</p> <p>---</p>	1-28
A	<p>O'HARE M. ET AL.: "Cytotoxicity of a recombinant ricin-A-chain fusion protein containing a proteolytically-cleavable spacer sequence" FEBS LETTERS, vol. 273, no. 1,2, 29 October 1990, pages 200-204, XP002041057 cited in the application see the whole document</p> <p>---</p>	1-28
A	<p>COOK J P ET AL: "BIOLOGICALLY ACTIVE INTERLEUKIN 2-RICIN A CHAIN FUSION PROTEINS MAY REQUIRE INTRACELLULAR PROTEOLYTIC CLEAVAGE TO EXHIBIT A CYTOTOXIC EFFECT" BIOCONJUGATE CHEMISTRY, vol. 4, no. 6, 1 November 1993, pages 440-447, XP000417282 see the whole document</p> <p>---</p>	1-28
A	<p>WO 89 01037 A (CETUS CORP) 9 February 1989 see the whole document</p> <p>-----</p>	1-28

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/CA 97/00288

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
Remark: Although claim(s) 21-24  
is(are) directed to a method of treatment of the human/animal  
body, the search has been carried out and based on the alleged  
effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such  
an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all  
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment  
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report  
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is  
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/CA 97/00288

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 0466222 A	15-01-92	US 5248606 A	28-09-93
		AU 638133 B	17-06-93
		AU 7832991 A	12-12-91
		CA 2044201 A	12-12-91
		CN 1062172 A	24-06-92
		JP 4279599 A	05-10-92
		US 5635384 A	03-06-97
		US 5646026 A	08-07-97
-----			
WO 8901037 A	09-02-89	AU 2136788 A	01-03-89
-----			